

SCORE Search Results Details for Application 10552515 and Search Result 20080624_083148_us-10-552-515-1.rup.

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This page gives you Search Results detail for the Application 10552515 and Search Result 20080624_083148_us-10-552-515-1.rup.

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GenCore version 6.2.1
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OM protein - protein search, using sw model

Run on: June 24, 2008, 08:32:16 ; Search time 518 Seconds
(without alignments)
2963.070 Million cell updates/sec

Title: US-10-552-515-1
Perfect score: 4950
Sequence: 1 MRMAATAWAGLQGPPPLTLC.....SELSSHWTPFTVPKASQLQQ 933

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 5032670 seqs, 1645091341 residues

Total number of hits satisfying chosen parameters: 5032670

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_12.1:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	4950	100.0	933	1 TM16G_HUMAN	Q6iwh7 homo sapien
2	3771.5	76.2	859	1 TM16G_MOUSE	Q14at5 mus musculus

3	3764	76.0	860	1	TM16G_RAT	Q6ift6	rattus norv
4	1539.5	31.1	920	2	A6QLE6_BOVIN	A6ql66	bos taurus
5	1525.5	30.8	903	2	Q1AP36_STRPU	Q1ap36	strongyloce
6	1525.5	30.8	955	1	TM16D_HUMAN	Q32m45	homo sapien
7	1523	30.8	921	2	Q1AP35_STRPU	Q1ap35	strongyloce
8	1512.5	30.6	981	2	A2AHE5_MOUSE	A2ahe5	mus musculus
9	1504	30.4	981	1	TM16C_HUMAN	Q3byt9	homo sapien
10	1500.5	30.3	900	2	A1A5Z4_DANRE	A1a5z4	danio rerio
11	1497	30.2	921	2	Q1AP37_STRPU	Q1ap37	strongyloce
12	1489	30.1	960	1	TM16A_MOUSE	Q8bh93	mus musculus
13	1482	29.9	986	1	TM16A_HUMAN	Q5xxa6	homo sapien
14	1467.5	29.6	913	2	Q8CFW1_MOUSE	Q8cfw1	mus musculus
15	1464	29.6	999	1	TM16B_HUMAN	Q9nq90	homo sapien
16	1455	29.4	913	1	TM16E_HUMAN	Q75v66	homo sapien
17	1449	29.3	896	2	Q6DDQ3_XENLA	Q6ddq3	xenopus lae
18	1448.5	29.3	1014	2	Q175J3_AEDAE	Q175j3	aedes aegyp
19	1445	29.2	1219	2	Q9VTS0_DROME	Q9vts0	drosophila
20	1443	29.2	1235	2	Q2M0Y5_DROPS	Q2m0y5	drosophila
21	1438.5	29.1	1117	2	Q0IEX5_AEDAE	Q0iex5	aedes aegyp
22	1433	28.9	906	2	Q7QDY0_ANOGA	Q7qdy0	anopheles g
23	1402.5	28.3	910	1	TM16F_HUMAN	Q4kmq2	homo sapien
24	1402	28.3	904	1	TM16E_MOUSE	Q75ur0	mus musculus
25	1402	28.3	904	2	Q3V657_MOUSE	Q3v657	mus musculus
26	1389	28.1	909	2	A6NNM6_HUMAN	A6nnm6	homo sapien
27	1384	28.0	1613	2	Q4S1F6_TETNG	Q4s1f6	tetraodon n
28	1383.5	27.9	871	2	Q8JFT1_DANRE	Q8jft1	danio rerio
29	1382.5	27.9	412	2	Q4SC97_TETNG	Q4sc97	tetraodon n
30	1371	27.7	911	1	TM16F_MOUSE	Q6p9j9	mus musculus
31	1369.5	27.7	1075	2	Q9VDV4_DROME	Q9vdrv4	drosophila
32	1367.5	27.6	712	2	Q8NCT7_HUMAN	Q8nct7	homo sapien
33	1367.5	27.6	926	2	Q8IN71_DROME	Q8in71	drosophila
34	1366.5	27.6	972	2	Q86P24_DROME	Q86p24	drosophila
35	1354	27.4	1062	2	Q293M2_DROPS	Q293m2	drosophila
36	1333	26.9	895	2	Q16L02_AEDAE	Q16l02	aedes aegyp
37	1319	26.6	1035	2	Q4SSV5_TETNG	Q4ssv5	tetraodon n
38	1306	26.4	863	2	Q16MH2_AEDAE	Q16mh2	aedes aegyp
39	1290	26.1	823	2	Q7QEP9_ANOGA	Q7qep9	anopheles g
40	1269	25.6	1017	2	Q29H97_DROPS	Q29h97	drosophila
41	1254.5	25.3	854	2	Q2VPA8_MOUSE	Q2vpa8	mus musculus
42	1249	25.2	984	2	Q8MT62_DROME	Q8mt62	drosophila
43	1237.5	25.0	971	2	Q4REV7_TETNG	Q4rev7	tetraodon n
44	1199.5	24.2	1043	2	Q9VYS8_DROME	Q9vys8	drosophila
45	1199.5	24.2	1059	2	Q76NS2_DROME	Q76ns2	drosophila

ALIGNMENTS

RESULT 1

TM16G_HUMAN

ID TM16G_HUMAN Reviewed; 933 AA.

AC Q6IWH7; Q6IWH6;

DT 29-MAY-2007, integrated into UniProtKB/Swiss-Prot.

DT 05-JUL-2004, sequence version 1.

DT 24-JUL-2007, entry version 21.

DE Transmembrane protein 16G (New gene expressed in prostate) (Prostate

DE cancer-associated protein 5) (IPCA-5) (Dresden-transmembrane protein
DE of the prostate) (D-TMPP).

GN Name=TMEM16G; Synonyms=NGEP, PCANAP5;
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 2), TISSUE SPECIFICITY,
RP SUBCELLULAR LOCATION, AND TOPOLOGY.
RX PubMed=14981236; DOI=10.1073/pnas.0308746101;
RA Bera T.K., Das S., Maeda H., Beers R., Wolfgang C.D., Kumar V.,
RA Hahn Y., Lee B., Pastan I.;
RT "NGEP, a gene encoding a membrane protein detected only in prostate
RT cancer and normal prostate.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:3059-3064(2004).
RN [2]
RP IDENTIFICATION.
RX PubMed=10613842; DOI=10.1101/gr.9.12.1198;
RA Walker M.G., Volkmuth W., Sprinzak E., Hodgson D., Klingler T.;
RT "Prediction of gene function by genome-scale expression analysis:
RT prostate cancer-associated genes.";
RL Genome Res. 9:1198-1203(1999).
RN [3]
RP IDENTIFICATION.
RX PubMed=15375614;
RA Katoh M., Katoh M.;
RT "Characterization of human TMEM16G gene in silico.";
RL Int. J. Mol. Med. 14:759-764(2004).
RN [4]
RP ALTERNATIVE SPLICING (ISOFORM 3), TISSUE SPECIFICITY, AND INDUCTION BY
RP ANDROGEN.
RX PubMed=15761874; DOI=10.1002/pros.20250;
RA Kiessling A., Weigle B., Fuessel S., Ebner R., Meye A., Rieger M.A.,
RA Schmitz M., Temme A., Bachmann M., Wirth M.P., Rieber E.P.;
RT "D-TMPP: a novel androgen-regulated gene preferentially expressed in
RT prostate and prostate cancer that is the first characterized member of
RT an eukaryotic gene family.";
RL Prostate 64:387-400(2005).
RN [5]
RP FUNCTION, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RX PubMed=17308099; DOI=10.1158/0008-5472.CAN-06-2673;
RA Das S., Hahn Y., Nagata S., Willingham M.C., Bera T.K., Lee B.,
RA Pastan I.;
RT "NGEP, a prostate-specific plasma membrane protein that promotes the
RT association of LNCaP cells.";
RL Cancer Res. 67:1594-1601(2007).
CC -!- FUNCTION: May play a role in cell-cell interactions.
CC -!- SUBCELLULAR LOCATION: Isoform 1: Cell membrane; Multi-pass
CC membrane protein. Isoform 2: Cytoplasm, cytosol. Note=Isoform 1
CC concentrates at sites of cell-cell contact.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1; Synonyms=NGEP-L;

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CC      IsoId=Q6IWH7-1; Sequence=Displayed;
CC      Name=2; Synonyms=NGEP-S;
CC      IsoId=Q6IWH7-2; Sequence=VSP_026004, VSP_026005, VSP_026006;
CC      Name=3; Synonyms=D-TMPP;
CC      IsoId=Q6IWH7-3; Sequence=VSP_026004, VSP_026007, VSP_026008;
CC      -!- TISSUE SPECIFICITY: Specifically expressed in epithelial cells of
CC      the prostate (at protein level).
CC      -!- INDUCTION: Up-regulated by androgen.
CC      -!- SIMILARITY: Belongs to the TMEM16 family.
CC      -!- CAUTION: It is uncertain whether Met-1 or Met-55 is the initiator.
CC      -----
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NoDerivs License
CC      -----
DR      EMBL; AY617079; AAT40139.1; -; mRNA.
DR      EMBL; AY617080; AAT40140.1; -; mRNA.
DR      UniGene; Hs.163909; -.
DR      Ensembl; ENSG00000146205; Homo sapiens.
DR      HGNC; HGNC:31677; TMEM16G.
DR      MIM; 605096; gene.
DR      PharmGKB; PA32980; -.
DR      ArrayExpress; Q6IWH7; -.
DR      GO; GO:0005886; C:plasma membrane; IDA:MGI.
DR      InterPro; IPR007632; DUF590.
DR      PANTHER; PTHR12308; DUF590; 1.
DR      Pfam; PF04547; DUF590; 1.
PE      1: Evidence at protein level;
KW      Alternative splicing; Cytoplasm; Membrane; Polymorphism;
KW      Transmembrane.
FT      CHAIN          1           933           Transmembrane protein 16G.
FT                                                         /FTId=PRO_0000289326.
FT      TOPO_DOM        1           355           Extracellular (Potential).
FT      TRANSMEM        356         376           Potential.
FT      TOPO_DOM        377         420           Cytoplasmic (Potential).
FT      TRANSMEM        421         441           Potential.
FT      TOPO_DOM        442         499           Extracellular (Potential).
FT      TRANSMEM        500         520           Potential.
FT      TOPO_DOM        521         550           Cytoplasmic (Potential).
FT      TRANSMEM        551         571           Potential.
FT      TOPO_DOM        572         588           Extracellular (Potential).
FT      TRANSMEM        589         609           Potential.
FT      TOPO_DOM        610         714           Cytoplasmic (Potential).
FT      TRANSMEM        715         735           Potential.
FT      TOPO_DOM        736         763           Extracellular (Potential).
FT      TRANSMEM        764         784           Potential.
FT      TOPO_DOM        785         843           Cytoplasmic (Potential).
FT      TRANSMEM        844         864           Potential.
FT      TOPO_DOM        865         933           Extracellular (Potential).
FT      VAR_SEQ         110         110           Missing (in isoform 2 and isoform 3).
FT                                                         /FTId=VSP_026004.
FT      VAR_SEQ         158         180           QDVQDGNITTVHYALLSASWAVLC -> VRGGCHGQGPRPCI
FT      HSVTHDLAA (in isoform 2).
FT                                                         /FTId=VSP_026005.
FT      VAR_SEQ         181         933           Missing (in isoform 2).
FT                                                         /FTId=VSP_026006.
FT      VAR_SEQ         859         859           H -> VAEAPAGSPIHGMRPRPCALPNSSTW (in

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FT isoform 3).
 FT /FTId=VSP_026007.
 FT VAR_SEQ 860 933 Missing (in isoform 3).
 FT /FTId=VSP_026008.
 FT VARIANT 67 67 V -> I (in dbSNP:rs2302054).
 FT /FTId=VAR_032616.
 SQ SEQUENCE 933 AA; 105531 MW; D6FD42578A41D7D3 CRC64;

Query Match 100.0%; Score 4950; DB 1; Length 933;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 933; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRMAATAWAGLQGPPLPTLCPAVRTGLYCRDQAHAEERWAMTSETSSGSHCARSRMLRRRA 60
 |||
 Db 1 MRMAATAWAGLQGPPLPTLCPAVRTGLYCRDQAHAEERWAMTSETSSGSHCARSRMLRRRA 60

Qy 61 QEEDSTVLIDVSPPEAEKRGSYGSTAHASEPGGQAAACRAGSPAKPRIADFLVWHEEL 120
 |||
 Db 61 QEEDSTVLIDVSPPEAEKRGSYGSTAHASEPGGQAAACRAGSPAKPRIADFLVWHEEL 120

Qy 121 KLDRQDQSAARDRTDMHRTWRETFDNLRAAGLCVDQDQDQDQDNTVHYALLSASWAVLC 180
 |||
 Db 121 KLDRQDQSAARDRTDMHRTWRETFDNLRAAGLCVDQDQDQDQDNTVHYALLSASWAVLC 180

Qy 181 YYAEDLRLKLPQLPQASNWSAGLLAWLGIPNVLLVVPDVPPEYYSRFRVKNLPRF 240
 |||
 Db 181 YYAEDLRLKLPQLPQASNWSAGLLAWLGIPNVLLVVPDVPPEYYSRFRVKNLPRF 240

Qy 241 LGSDNQDTFFTSTKRHQLFEILAKTPYGHEKKNLLGIHQLLAEGVLSAAFPPLHDGPFKT 300
 |||
 Db 241 LGSDNQDTFFTSTKRHQLFEILAKTPYGHEKKNLLGIHQLLAEGVLSAAFPPLHDGPFKT 300

Qy 301 PPEGQPAPRLNQRQVLFQHWARWGKWKYQPLDHVRRYFGEKVALYFAWLGFYTGWLLPA 360
 |||
 Db 301 PPEGQPAPRLNQRQVLFQHWARWGKWKYQPLDHVRRYFGEKVALYFAWLGFYTGWLLPA 360

Qy 361 AVVGLTVLVGCFVFSDIPTQELCGSKDSFEMCPLCLDCPFWLLSSACALAQAGRLFDH 420
 |||
 Db 361 AVVGLTVLVGCFVFSDIPTQELCGSKDSFEMCPLCLDCPFWLLSSACALAQAGRLFDH 420

Qy 421 GGTVFFSLFMALWAVLLEWYKRKSATLAYRWDCSDYEDTEERPRPQFAASAPMTAPNPI 480
 |||
 Db 421 GGTVFFSLFMALWAVLLEWYKRKSATLAYRWDCSDYEDTEERPRPQFAASAPMTAPNPI 480

Qy 481 TGEDEPYFPERSRARRMLAGSVVIVVMVAVVVMCLVSIILYRAIMAVVSRSGNTLLAAW 540
 |||
 Db 481 TGEDEPYFPERSRARRMLAGSVVIVVMVAVVVMCLVSIILYRAIMAVVSRSGNTLLAAW 540

Qy 541 ASRIASLTGSVNVNLFILILSKIYVSLAHVLTWEMHRTQTKFEDAFTLKVFIFQFVNFY 600
 |||
 Db 541 ASRIASLTGSVNVNLFILILSKIYVSLAHVLTWEMHRTQTKFEDAFTLKVFIFQFVNFY 600

Qy 601 SSPVYIAFFKGRFVGYPGNYHTLFGVRNEECAAGGCLIELAQELLVIMVGKQVINNMQEV 660
 |||
 Db 601 SSPVYIAFFKGRFVGYPGNYHTLFGVRNEECAAGGCLIELAQELLVIMVGKQVINNMQEV 660

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Qy      661  LIPKLGWQKFRRLRSKKRKAGASAGASQGPWEDDYELVPCEGLFDEYLEMVLQFGFVTI  720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661  LIPKLGWQKFRRLRSKKRKAGASAGASQGPWEDDYELVPCEGLFDEYLEMVLQFGFVTI  720

Qy      721  FVAACPLAPLFA LLNNWVEIRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVISN  780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721  FVAACPLAPLFA LLNNWVEIRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVISN  780

Qy      781  AFL LAFSSDFLPRAYYRWTRAHDLRGFLNFTLARAPSSFAAHHNRTCryRAFRDDGHYS  840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781  AFL LAFSSDFLPRAYYRWTRAHDLRGFLNFTLARAPSSFAAHHNRTCryRAFRDDGHYS  840

Qy      841  QTYWNL LAILRAFVIVFEHV VFSVGRLLDLLVPDIPESVEIKVKREYYLAKQALAENEVL  900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841  QTYWNL LAILRAFVIVFEHV VFSVGRLLDLLVPDIPESVEIKVKREYYLAKQALAENEVL  900

Qy      901  FGTNGTKDEQPKGSELSSHWPFTVPKASQLQQ  933
         ||||||||||||||||||||||||||||||||||
Db      901  FGTNGTKDEQPKGSELSSHWPFTVPKASQLQQ  933

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RESULT 2

TM16G_MOUSE

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ID      TM16G_MOUSE                      Reviewed;                      859 AA.
AC      Q14AT5; Q6IFT5;
DT      29-MAY-2007, integrated into UniProtKB/Swiss-Prot.
DT      29-MAY-2007, sequence version 2.
DT      24-JUL-2007, entry version 9.
DE      Transmembrane protein 16G (New gene expressed in prostate homolog).
GN      Name=Imem16g; Synonyms=Ngep;
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC      Muroidea; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC      STRAIN=C57BL/6J;
RG      The mouse genome sequencing consortium;
RL      Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN      [2]
RP      NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 2).
RX      PubMed=15489334; DOI=10.1101/gr.2596504;
RG      The MGC Project Team;
RT      "The status, quality, and expansion of the NIH full-length cDNA
RT      project: the Mammalian Gene Collection (MGC).";
RL      Genome Res. 14:2121-2127(2004).
RN      [3]
RP      IDENTIFICATION.
RX      PubMed=14981236; DOI=10.1073/pnas.0308746101;
RA      Bera T.K., Das S., Maeda H., Beers R., Wolfgang C.D., Kumar V.,
RA      Hahn Y., Lee B., Pastan I.;
RT      "NGEP, a gene encoding a membrane protein detected only in prostate
RT      cancer and normal prostate.";
RL      Proc. Natl. Acad. Sci. U.S.A. 101:3059-3064(2004).

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CC  -!- FUNCTION: May play a role in cell-cell interactions (By
CC      similarity).
CC  -!- SUBCELLULAR LOCATION: Cell membrane; Multi-pass membrane protein
CC      (By similarity). Note=Concentrates at sites of cell-cell contact
CC      (By similarity).
CC  -!- ALTERNATIVE PRODUCTS:
CC      Event=Alternative splicing; Named isoforms=2;
CC      Name=1;
CC      IsoId=Q14AT5-1; Sequence=Displayed;
CC      Name=2;
CC      IsoId=Q14AT5-2; Sequence=VSP_026009, VSP_026010;
CC  -!- SIMILARITY: Belongs to the TMEM16 family.
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CC  Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
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DR  EMBL; AC108412; -; NOT_ANNOTATED_CDS; Genomic_DNA.
DR  EMBL; AC124669; -; NOT_ANNOTATED_CDS; Genomic_DNA.
DR  EMBL; BC116706; AAI16707.1; -; mRNA.
DR  EMBL; BK004075; DAA04566.1; -; mRNA.
DR  UniGene; Mm.297411; -.
DR  Ensembl; ENSMUSG00000034107; Mus musculus.
DR  MGI; MGI:3052714; Tmem16g.
DR  InterPro; IPR007632; DUF590.
DR  PANTHER; PTHR12308; DUF590; 1.
DR  Pfam; PF04547; DUF590; 1.
PE  2: Evidence at transcript level;
KW  Alternative splicing; Membrane; Transmembrane.
FT  CHAIN          1           859           Transmembrane protein 16G.
FT                                     /FTId=PRO_0000289327.
FT  TOPO_DOM       1           297           Extracellular (Potential).
FT  TRANSMEM       298        318           Potential.
FT  TOPO_DOM       319        362           Cytoplasmic (Potential).
FT  TRANSMEM       363        383           Potential.
FT  TOPO_DOM       384        441           Extracellular (Potential).
FT  TRANSMEM       442        462           Potential.
FT  TOPO_DOM       463        492           Cytoplasmic (Potential).
FT  TRANSMEM       493        513           Potential.
FT  TOPO_DOM       514        530           Extracellular (Potential).
FT  TRANSMEM       531        551           Potential.
FT  TOPO_DOM       552        651           Cytoplasmic (Potential).
FT  TRANSMEM       652        672           Potential.
FT  TOPO_DOM       673        700           Extracellular (Potential).
FT  TRANSMEM       701        721           Potential.
FT  TOPO_DOM       722        780           Cytoplasmic (Potential).
FT  TRANSMEM       781        801           Potential.
FT  TOPO_DOM       802        859           Extracellular (Potential).
FT  VAR_SEQ        836        843           ALLGATGV -> VTVGVTGG (in isoform 2).
FT                                     /FTId=VSP_026009.
FT  VAR_SEQ        844        859           Missing (in isoform 2).
FT                                     /FTId=VSP_026010.
SQ  SEQUENCE      859 AA;  97128 MW;  82E1A473C59C8DA3 CRC64;

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Query Match 76.2%; Score 3771.5; DB 1; Length 859;
 Best Local Similarity 83.0%; Pred. No. 1e-300;

Matches	716;	Conservative	43;	Mismatches	95;	Indels	9;	Gaps	4;
Qy	55	MLRRRAQEEDSTVLIDVSPPEAEKRGSYGTAHASEPGGQQAACRAGSPAKPRIADFVL	114	: : ::					
Db	1	MLRGQAREEDSVVLIDMASPEAGNGCSYGTAAQASEAGKQVAPSRVSGSSAKPPI-DFVL	59						
Qy	115	VWEEDLKLDRQDQSAARDRTDMHRTWRETFLDNLRAGLCVDQDQDVQDGNNTVHYALLSA	174	: : : : : :					
Db	60	VWEEDL---RNQENPTKDKTDTHEVWRETFLNCLAGLKIDQHDVQDEAAAVHYILLRA	116						
Qy	175	SWAVLCYYAEDLRLLKLPLQELPNQASNWSAGLLAWLGIPNVLLLEVVPDPVPEYYSCRFRV	234						
Db	117	PWAVLCYYAEDLRLLKLPLQELPNQASNWSATLLEWLGIPIILHVPDTPPEYYSCQFKA	176						
Qy	235	NKLPRFLGSDNQDTFTTSTKRHQILFEILAKTPYGHEKKNLGLIHLQALLAEGVLSAAFPFLH	294	:					
Db	177	SKLQWFLGSDNQDTFTTSTKRHQILFEILAKTPYGHEKKGLFGIDQLLAEGVLSAAFPFLH	236						
Qy	295	DGPFKTPPEGPQAPRLNQRQVLFQHWARWGKWNKYQPLDHVRRYFGEKVALYFAWLGFYT	354						
Db	237	DGPFSAVPESSQVGLGIQRQVLFQHWARWGKWNKYQPLDHVRRYFGEKVALYFAWLGFYT	296						
Qy	355	GWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGSKDSFEMCPLCLDCPFWLLSSACALQA	414						
Db	297	GWLLPAAVVGTVVFLVGCFLVFSDIPTQELCHSSDSFDMCPLCSDCSFWLLSSACTLAQA	356						
Qy	415	GRLFDHGGTVFFSLFMALWAVLLLEYWKRKSATLAYRWDCSDYEDTEERPRPQFAASAPM	474						
Db	357	GRLFDHGGTVFFSLFMALWAVLLLEYWKRKNATLAYRWDCSDYEDIEERPRPQFAATAPM	416						
Qy	475	TAPNPITGEDEPYFFPERSARRMLAGSVVIVVMVAVVVMCLVSIILYRAIMAIIVSRSGN	534						
Db	417	TALNPITGEDEPYFPEKNRVRMLAGSVVLLMMVAVVIMCLVSVILYRAVMAIIVSRSDN	476						
Qy	535	TLAAWASRIASLTGVSNNLVFILILSKIYVSLAHVLTWRWEMHRTQTKEFADFTLVKFIF	594	:					
Db	477	AFLSAWASRIASLTGVSNNLVFILILSKVYVLLAQVLTWRWEMHRTQTKEFADFTLVKFIF	536						
Qy	595	QVNFYSSPVYIAFFKGRFVGYPGNYHTLFGVRNEECAAGGCLIELAQELLVIMVGKQVI	654	:					
Db	537	QVNFYASPVYIAFFKGRFVGYPGNYHTLFGIRNEECAPAGGCLSELAQELLVIMVGKQII	596						
Qy	655	NNMQEVLIPKLKGWQKFRRLRSKKRKAGASAGSQGPWEDDYELVPCEGLFDEYLEMVLQ	714	:					
Db	597	NNVQEVLPVKLKGWQKF---SRGKKAG--TGTHAPWEADYELLPCEGLFHEYLEMVLQ	651						
Qy	715	FGFVTIFVAACPLAPLALLNNWVEIRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTH	774						
Db	652	FGFVTIFVAACPLAPLALLNNWVEIRLDARKFVCEYRRPVAERAQDIGIWFHILTGLTH	711						
Qy	775	LAVISNAFLAFSSDFLPRAYYRWTRAHDLRGFLNFTLARAPSSFAAAHNRTCERYRAFRD	834						
Db	712	LAVISNAFLAFSSDFLPRVYYSWTHAPDLHGFLNFTLARAPPTFTSAHNRTCERYRAFRD	771						
Qy	835	DDGHYSQTYWNLLAIRLAFVIVFEHVVSFVGRLLDLLVPDIPESVEIKVKREYYLAKQAL	894						

Dd 772 DDGHYSPTYWTLAILRALFVIVFEHVVSIGRVLDDLVPDIPESVEIKVKREYYLAKQAL 831

Qy 895 AENEVLFGTNGTKDEQPKGSELS 917
 |||| | | | ||:| | | |

Dd 832 AENEALLGATGVKDDQPPSSEPS 854

RESULT 3

TM16G_RAT

ID TM16G_RAT Reviewed; 860 AA.

AC Q6IFT6;

DT 29-MAY-2007, integrated into UniProtKB/Swiss-Prot.

DT 05-JUL-2004, sequence version 1.

DT 24-JUL-2007, entry version 22.

DE Transmembrane protein 16G (New gene expressed in prostate homolog).

GN Name=Trm16g; Synonyms=Ngep;

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muroidea; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=Brown Norway;

RX PubMed=15057822; DOI=10.1038/nature02426;

RA Gibbs R.A., Weinstock G.M., Metzker M.L., Muzny D.M., Sodergren E.J.,

RA Scherer S., Scott G., Steffen D., Worley K.C., Burch P.E., Okwuonu G.,

RA Hines S., Lewis L., Deramo C., Delgado O., Dugan-Rocha S., Miner G.,

RA Morgan M., Hawes A., Gill R., Holt R.A., Adams M.D., Amanatides P.G.,

RA Baden-Tillson H., Barnstead M., Chin S., Evans C.A., Ferriera S.,

RA Fosler C., Glodok A., Gu Z., Jennings D., Kraft C.L., Nguyen T.,

RA Pfannkuch C.M., Sitter C., Sutton G.G., Venter J.C., Woodage T.,

RA Smith D., Lee H.-M., Gustafson E., Cahill P., Kana A.,

RA Doucette-Stamm L., Weinstock K., Fechtel K., Weiss R.B., Dunn D.M.,

RA Green E.D., Blakesley R.W., Bouffard G.G., De Jong P.J., Osogawa K.,

RA Zhu B., Marra M., Schein J., Bosdet I., Fjell C., Jones S.,

RA Krzywinski M., Mathewson C., Siddiqui A., Wye N., McPherson J.,

RA Zhao S., Fraser C.M., Shetty J., Shatsman S., Geer K., Chen Y.,

RA Abramson S., Nierman W.C., Havlak P.H., Chen R., Durbin K.J., Egan A.,

RA Ren Y., Song X.-Z., Li B., Liu Y., Qin X., Cawley S., Cooney A.J.,

RA D'Souza L.M., Martin K., Wu J.Q., Gonzalez-Garay M.L., Jackson A.R.,

RA Kalafus K.J., McLeod M.P., Milosavljevic A., Virk D., Volkov A.,

RA Wheeler D.A., Zhang Z., Bailey J.A., Eichler E.E., Tuzun E.,

RA Birney E., Mongin E., Ureta-Vidal A., Woodward C., Zdobnov E.,

RA Bork P., Suyama M., Torrents D., Alexandersson M., Trask B.J.,

RA Young J.M., Huang H., Wang H., Xing H., Daniels S., Gietzen D.,

RA Schmidt J., Stevens K., Vitt U., Wingrove J., Camara F., Mar Alba M.,

RA Abril J.F., Guigo R., Smit A., Dubchak I., Rubin E.M., Couronne O.,

RA Poliakov A., Huebner N., Ganten D., Goesele C., Hummel O.,

RA Kreitler T., Lee Y.-A., Monti J., Schulz H., Zimdahl H.,

RA Himmelbauer H., Lehrach H., Jacob H.J., Bromberg S.,

RA Gullings-Handley J., Jensen-Seaman M.I., Kwitek A.E., Lazar J.,

RA Pasko D., Tonellato P.J., Twigger S., Ponting C.P., Duarte J.M.,

RA Rice S., Goodstadt L., Beatson S.A., Emes R.D., Winter E.E.,

RA Webber C., Brandt P., Nyakatura G., Adetobi M., Chiaromonte F.,

RA Elnitski L., Eswara P., Hardison R.C., Hou M., Kolbe D., Makova K.,
RA Miller W., Nekrutenko A., Riemer C., Schwartz S., Taylor J., Yang S.,
RA Zhang Y., Lindpaintner K., Andrews T.D., Caccamo M., Clamp M.,
RA Clarke L., Curwen V., Durbin R.M., Eyraas E., Searle S.M., Cooper G.M.,
RA Batzoglou S., Brudno M., Sidow A., Stone E.A., Payseur B.A.,
RA Bourque G., Lopez-Otin C., Puente X.S., Chakrabarti K., Chatterji S.,
RA Dwey C., Pachter L., Bray N., Yap V.B., Caspi A., Tesler G.,
RA Pevzner P.A., Haussler D., Roskin K.M., Baertsch R., Clawson H.,
RA Furey T.S., Hinrichs A.S., Karolchik D., Kent W.J., Rosenbloom K.R.,
RA Trumbower H., Weirauch M., Cooper D.N., Stenson P.D., Ma B., Brent M.,
RA Arumugam M., Shteynberg D., Copley R.R., Taylor M.S., Riethman H.,
RA Mudunuri U., Peterson J., Guyer M., Felsenfeld A., Old S., Mockrin S.,
RA Collins F.S.;
RT "Genome sequence of the Brown Norway rat yields insights into
RT mammalian evolution.";
RL Nature 428:493-521(2004).
RN [2]
RP IDENTIFICATION.
RX PubMed=14981236; DOI=10.1073/pnas.0308746101;
RA Bera T.K., Das S., Maeda H., Beers R., Wolfgang C.D., Kumar V.,
RA Hahn Y., Lee B., Pastan I.;
RT "NGEP, a gene encoding a membrane protein detected only in prostate
RT cancer and normal prostate.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:3059-3064(2004).
CC -!- FUNCTION: May play a role in cell-cell interactions (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Cell membrane; Multi-pass membrane protein
CC (By similarity). Note=Concentrates at sites of cell-cell contact
CC (By similarity).
CC -!- SIMILARITY: Belongs to the TMEM16 family.

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DR EMBL; AABR03068351; -; NOT_ANNOTATED_CDS; Genomic_DNA.
DR EMBL; AABR03069029; -; NOT_ANNOTATED_CDS; Genomic_DNA.
DR EMBL; AABR03070767; -; NOT_ANNOTATED_CDS; Genomic_DNA.
DR EMBL; BK004074; DAA04565.1; -; mRNA.
DR UniGene; Rn.163084; -.
DR Ensembl; ENSRNOG00000023427; Rattus norvegicus.
DR RGD; 1302987; Ngep.
DR InterPro; IPR007632; DUF590.
DR PANTHER; PTHR12308; DUF590; 1.
DR Pfam; PF04547; DUF590; 1.
PE 2: Evidence at transcript level;
KW Membrane; Transmembrane.
FT CHAIN 1 860 Transmembrane protein 16G.
FT /FTId=PRO_0000289328.
FT TOPO_DOM 1 297 Extracellular (Potential).
FT TRANSMEM 298 318 Potential.
FT TOPO_DOM 319 362 Cytoplasmic (Potential).
FT TRANSMEM 363 383 Potential.
FT TOPO_DOM 384 441 Extracellular (Potential).
FT TRANSMEM 442 462 Potential.
FT TOPO_DOM 463 492 Cytoplasmic (Potential).
FT TRANSMEM 493 513 Potential.

FT	TOPO_DOM	514	530	Extracellular (Potential).
FT	TRANSMEM	531	551	Potential.
FT	TOPO_DOM	552	652	Cytoplasmic (Potential).
FT	TRANSMEM	653	673	Potential.
FT	TOPO_DOM	674	701	Extracellular (Potential).
FT	TRANSMEM	702	722	Potential.
FT	TOPO_DOM	723	779	Cytoplasmic (Potential).
FT	TRANSMEM	780	800	Potential.
FT	TOPO_DOM	801	860	Extracellular (Potential).
SQ	SEQUENCE	860 AA;	97170 MW;	96BE3CBD6DE96101 CRC64;

Query Match 76.0%; Score 3764; DB 1; Length 860;

Best Local Similarity 82.7%; Pred. No. 4.3e-300;

Matches 714; Conservative 47; Mismatches 94; Indels 8; Gaps 4;

Qy	55	MLRRRAQEEDSTVLIDVSPPEAEKRGSYGSTAHASEPGGQQAACRAGSPAKPRIADFVL	114
		:: ::	
Db	1	MLRKQAGEEDSVVLIDMTSPEAGNGCSYGSTAQASEAGKQVAPSRVGSANPPI--DFVL	59
Qy	115	VWEEDLKLDRQDQSAARDRTDMHRTWRETFLDNLRAGLCVDQDQDGNNTVHYALLSA	174
		::: : :: : :	
Db	60	VWEEDL---RSRENPTQDKTDTHEIWRETFLNLRVAGLKIDQRDQDEAAAVHYILLSA	116
Qy	175	SWAVLCYYAEDLRKLPLQELPNQASNWSAGLLAWLGIPNVLLLEVDPVPPEYYSRFRV	234
Db	117	PWAVLCYYAEDLRKLPLQELPNQASNWSATLLEWLGIPNILLNVDPDTPPEYYSQFKA	176
Qy	235	NKLPRFLGSDNQDTFTTSTKRHQILFEILAKTPYGHKEKNLLGIHQLLAEGVLSAAFPPLH	294
		:	
Db	177	SKLQWFLGSDNQDTFTTSTKRHQILFEILAKTPYGHQKGLFGIDQLAEGVLSAAFPPLH	236
Qy	295	DGPFKTPPEGPQAPRLNQRQVLFQHWARWGKWNKYQPLDHVRRYFGEKVALYFAWLGFYT	354
		:	
Db	237	DGPFVVPPESSQVLGLTQRQVLFKHARWGKWRKYQPLDHVRRYFGEKVALYFAWLGFYT	296
Qy	355	GWLLPAAVVGTLVFLVGLGCVLFVSDIPTQELCGSKDSFEMCPLCLDCPFWLLSSACALQA	414
		: : :	
Db	297	GWLLPAAVVGTVVFLAGCFLVFSVPTQELCHSSDTFDMCPLCSDCSFWLLSSACTLAQA	356
Qy	415	GRLFDHGGTVFFSLFMALWAVLLELYWKRKSATLAYRWDCSDYEDTEERPRPQFAASAPM	474
Db	357	GRLFDHGGTVFFSLFMALWAVLLELYWKRKNATLAYRWDCSDYEDTEERPRPQFAATAPM	416
Qy	475	TAPNPITGEDEPYFPERSRARRMLAGSVVIVVMVAVVVMCLVSIILYRAIMAIIVSRSGN	534
		: : : :	
Db	417	TALNPITGEDEPYFPEKNRVRMLAGSVVLLMMVAVVIMCLVSIILYRAVMAIIVSKSN	476
Qy	535	TLLAAWASRIASLTGSVVNLVFIILSKIYVSLAHVLTREWMHRTQTQKFEDAFTLKVFIF	594
		: :	
Db	477	AFLSAWASRIASLTGSVVNLVFIILSKVYVILAQVLTREWMHRTQTAFEDAFTLKVFIF	536
Qy	595	QFVNFYSSPVYIAFFKGRFVGYPGNYHTLFGVRNEECAAGGLIELAQELLVIMVGKQVI	654
		:	
Db	537	QFVNFYASPVYIAFFKGRFVGYPGNYHTLFGVRNEECAGGCLSELAQELLVIMVGKQII	596

```

Qy      655 NNMQEVLPKLPKLGWQKFRRLRSKKRKAGASAGASQGPWEDDYELVPCGLGFDEYLEMVLQ 714
      ||:||||:||||| ||| ||::||| ||: ||| ||||:||||| |||||
Db      597 NNVQEVLPKLPKLGWCQK--LCSRRKKAG--MGANPAPWEADYELLPCEGLGFHEYLEMVLQ 652

Qy      715 FGFVTIFVAACPLAPLAFALLNNWVEIRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTH 774
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      653 FGFVTIFVAACPLAPLAFALLNNWVEIRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTH 712

Qy      775 LAVISNAFLAFSSDFLPRAYYRWTRAHDLRGFLNFTLARAPSSFAAAHNRTCryAFRD 834
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      713 LAVISNAFLAFSSDFLPRVYYSWTRAPDLRGFLNFTLARAPPTFTSAHNRTCryAFRD 772

Qy      835 DDGHYSQTYWNLLAIRLAFVIVFEHVVSFVGRLLDLLVPDIPESVEIKVKREYYLAKQAL 894
      ||||| ||| ||||| ||||| ||| ||||| ||||| ||||| ||||| |||||
Db      773 DDGHYSPTYWTLAIRLAFVIVFEHVVSFSTGRFLDLLVPDIPESVEIKVKREYYLAKQAL 832

Qy      895 AENEVLFGTNGTKDEQPKGSELS 917
      |:||| || |||| |||
Db      833 ADNEALLGATGVKGEQPPSSEPS 855

```

RESULT 4

A6QLE6_BOVIN

```

ID      A6QLE6_BOVIN                      Unreviewed;          920 AA.
AC      A6QLE6;
DT      21-AUG-2007, integrated into UniProtKB/TrEMBL.
DT      21-AUG-2007, sequence version 1.
DT      21-AUG-2007, entry version 1.
DE      Putative uncharacterized protein.
OS      Bos taurus (Bovine).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC      Pecora; Bovidae; Bovinae; Bos.
OX      NCBI_TaxID=9913;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RC      STRAIN=L1 Hereford; TISSUE=Basal ganglia;
RA      Moore S., Alexander L., Brownstein M., Guan L., Lobo S., Meng Y.,
RA      Tanaguchi M., Wang Z., Yu J., Prange C., Schreiber K., Shenmen C.,
RA      Wagner L., Bala M., Barbazuk S., Barber S., Babakaiff R., Beland J.,
RA      Chun E., Del Rio L., Gibson S., Hanson R., Kirkpatrick R., Liu J.,
RA      Matsuo C., Mayo M., Santos R.R., Stott J., Tsai M., Wong D.,
RA      Siddiqui A., Holt R., Jones S.J., Marra M.A.;
RL      Submitted (JUN-2007) to the EMBL/GenBank/DBJ databases.
CC      -----
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CC      Distributed under the Creative Commons Attribution-NoDerivs License
CC      -----
DR      EMBL; BC147937; AAI47938.1; -; mRNA.
PE      2: Evidence at transcript level;
SQ      SEQUENCE      920 AA; 107708 MW; 3AFFC6310F1862CD CRC64;

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Query Match 31.1%; Score 1539.5; DB 2; Length 920;
 Best Local Similarity 37.8%; Pred. No. 6.7e-117;
 Matches 361; Conservative 166; Mismatches 311; Indels 117; Gaps 29;

Qy	44	TSSGSHCARSMRLRRRAQEEDSTVLID---VSPPEAE---KRGSYGST---AHASEP	91
Db	4	SSSGITNGRTRVHFHPVA--KDVNILFDELEAVNSPCKDDSLHHPGNLTSTSDDASRLEA	61
Qy	92	GGQQAACRAGSPAKPRI-----ADFVLVWEEDLKLDROQDASAARDRTDMHRTW	140
Db	62	GGETV-----PEKNKLNGLYFRDGKCRIDYILVYR---KSNPQMEK-----	99
Qy	141	RETFLDNLRAAGLCVDQDQVDQDGNNTTVHYALLSASWAVLCYYAEDLRKLPLQE---LP	196
Db	100	REVFERNIRAEGLOMEKESSLI-NSDIIFVKLHAPWEVLGRYAEQMNVMRMPFRKRIYYLP	158
Qy	197	NQASNWS-----AGLLAWLGIPNVLL---EVVPDVPP-EYYSRCFRVKNKLPRLGSDNQD	247
Db	159	RRYKFMSRIDKQISRFRRWLPKKPMRLDKETLPDLEENDCYTAPFSQORIHFFI-IHNKD	217
Qy	248	TFFTSTKRHQILFEILAKTPYGHEKKNLGIHQLLAEGVLSAAFPPLHDGPFKTPPEGPQA	307
Db	218	TFNNATRSRIVHHILQRIKY-EEGKNKIGLNRLLTNGSYEAAFPPLHEGSYRSKNSIRTH	276
Qy	308	PRLNQRQVLFQHWARWGKNKYQPLDHYRRYFGEKVAFWLGFTYTWLLPAAVVGTLV	367
Db	277	GAVNHRHLLYECWASGWWGYKYQPLDLVRRYFGEKIGLYFAWLGWYTGMLFPAAFIGLFV	336
Qy	368	FLVGCFLVFSDIPTQELCGSKDSFEMCPLC-LDCPFWLLSSACALAGRLFDHGGTVFF	426
Db	337	FLYGVITLDHCQVSKEVCQATDII-MCPVCDKCYCFMRLSDSCVYAKVTHLFDNGATVFF	395
Qy	427	SLFMALWAVLLLEYWKRKSATLAYRWDCSDYEDTEERPRPQFAAS-APMTAPNPITGEDE	485
Db	396	AVFMAVWATVLFLEFWKRRRAVIAYDWDLIDWEEEEEEIRPQFEAKYSKKERMNPNISGKPE	455
Qy	486	PYFPERSRARRMLAGSVVIVVMVAVVMCLVSIILYRAIMAIVRSRGNTLLA-AWA---	541
Db	456	PYQAFADKCSRLIVSASGIFFMICVIAAVFGIIVYRVVTV-----STFAAFKVALIR	508
Qy	542	--SRIASLTGSVV--NLVFILILSKIYVSLAHVLTWRWEMHRTQTKFEDAFTLKVFIFQFV	597
Db	509	NNSQVAT-TGTAVCINFCIIMLLNVLYEKVALLLTNLEQPRTESEWENSFTLKMFLFQFV	567
Qy	598	NFYSSPVYIAFFKGRFVGYPGNYHTLFG-VRNEECAAGGCLIELAQELLVIMVGQVINN	656
Db	568	NLNSSTFYIAFFLGRFTGHPGAYLRLINRWRLEECHPSGCLIDLCMQMGIIMVLKQTWNN	627
Qy	657	MQEVLIPLKLGWWQKFLRLSKRRKAGASAGASQGPWEDDYELVPCE--GLFDEYLEMVLQ	714
Db	628	FMELGPLYLIQNWVTR--RKVRQEHGPERKISFPQWEKDYNLQPMNAYGLFDEYLEMILQ	684
Qy	715	FGFVTIFVAACPLAPLALLNNWVEIRLDARKFVCEYRRPVAERAQDIGHFHLAGLTH	774
Db	685	FGFTTIFVAAPLAPLALLNNIIEIRLDAYKFVTQWRRLASRAKDIGHWYGILEGIGI	744
Qy	775	LAVISNAFLAFSSDFLPRAYRW-----TRAHDLRGLFNFTLA-----	813
Db	745	LSVITNAFVIAITSDFIPRLVYAYKYGPCAGQGEAGQKCMVGYNASLSVFRISDFENRS	804

```

Qy      814 ---RAPSSFAAAHNRTCryAFRDDDGH----YSQTYWNLLAIRLAFVIVFEHVVFVSVG 865
      | | : : ||| :|| | : :||| ||| :||| :||| :
Db      805 EPESDGESEFGTPLYKCYRDRYRPPHSLVPYGYTLQFHWHLAARLAFIIVFEHLVFCIK 864

Qy      866 RLLDLLVPDIPESVEIKVKREYYLAKQALAEVLFNGTKDEQPKGSELSSHW 920
      | : ||| : : : || || : : | | : : | : | : |
Db      865 HLISYLPDLPKDLRDRMRREKYLIQEMMYEAELERLQKERKERKKNKAHHNEW 919

```

RESULT 5

Q1AP36_STRPU

```

ID      Q1AP36_STRPU              Unreviewed;          903 AA.
AC      Q1AP36;
DT      11-JUL-2006, integrated into UniProtKB/TrEMBL.
DT      11-JUL-2006, sequence version 1.
DT      24-JUL-2007, entry version 6.
DE      122 kDa protein TMEM16 (Fragment).
OS      Strongylocentrotus purpuratus (Purple sea urchin).
OC      Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC      Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
OC      Strongylocentrotus.
OX      NCBI_TaxID=7668;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RC      TISSUE=Coelomocyte;
RA      Galindo B.E., Moy G.W., Vacquier V.D.;
RT      "A 122 kDa protein from Strongylocentrotus purpuratus embryo belongs
RT      to TMEM16 protein family.";
RL      Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
CC      -----
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CC      -----
DR      EMBL; DQ020165; AAY82886.1; -; mRNA.
DR      UniGene; Spu.15325; -.
DR      InterPro; IPR007632; DUF590.
DR      PANTHER; PTHR12308; DUF590; 1.
DR      Pfam; PF04547; DUF590; 1.
PE      2: Evidence at transcript level;
FT      NON_TER      1      1
SQ      SEQUENCE      903 AA; 104887 MW; 443A4A4A7E50074A CRC64;

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Query Match 30.8%; Score 1525.5; DB 2; Length 903;
 Best Local Similarity 38.1%; Pred. No. 9.3e-116;
 Matches 338; Conservative 161; Mismatches 304; Indels 85; Gaps 21;

```

Qy      61 QEEDSTVLIDVSPPEAEKRGSYGSTAHASEPGGQAAACRAGSPAK----- 106
      | ::| | :| | | : :| | : : ||||
Db      17 QPDNAAV---ANPQEIEM-----AESHMGAPTDKEDQPLHEGSPAKKDDNKVNDLFFKDG 68

Qy      107 PRIADFVLVWEEDLKLDRQQDSAAARDTDMHRTWRETFDLNLRAGLCVD---QQDVQDG 163
      | ||| : | :| | | : : | : | | || : : : ||
Db      69 KRRIDFVLAY-----RKQSEEREERKRVKK--RQNFLEANLDEGLQLEYENSESHDG 119

Qy      164 NTTVHYALLSASWAVLCYYAEDLRLKLPLQELPNQASNWSAGLLAWLGIPNVLLVVPDV 223

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      | : : | | :: |||:|::|::| : : | | | |
Db 120 RT--FFVKVHAPWDLMTRYAEELKIKMPIEENNMEEPVNVCIDKLWTFPELSEEVK 177

Qy 224 PPEYYSCFRVKNLPRFLGSDNQDTFFTSTKRHQILFEILAKTPYGHEKKNLLGIHQLLA 283
      |: :: | :: |: ::||| | : |:::| | : | || |:|
Db 178 EPDVTAPFIRDRASEFI--MESQDTFFPNINRNVVEILERMRYDANDPAKFGIDHLA 236

Qy 284 EGVLSAAFLHDGPFKTP---PEGQAPRLNQQLVQHWARGKWNKYQLPDHVVRYF 339
      | ||:| | : | : || | | : | : | | | | : || |
Db 237 NGSYFAAYPLHEGDYKSKHSLTHGPQ---NDRHLLYEWARPGRWYKKQPLDIRRYF 292

Qy 340 GEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGSKDSFEMCPLC-L 398
      ||| : | | | | | | | | | | | | | | | | | | | |
Db 293 GEKIGIYFCWLGFYTEMLTWAGFVGLIVFLYGCISLPSSVVVQEICDGTDI--MCPLCDK 351

Qy 399 DCPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLEYWKRKSATLAYRWDCSDYE 458
      ||:| || : | :: |||: |||: ||:| | : |::| : | || : |
Db 352 RCPYWTLSDCSFYKSLTYLFDNEATVFFACFMSLWATMCFEWFKRRQNTIDYDWDLFGFE 411

Qy 459 DTEERPRPQFAASAPMTAPNPITGEDEPYFPERSRARMLAGSVVIVVMVAVVMCLVSI 518
      : || ||:| | || : || | || : | | | | : : : :
Db 412 EQEENIRPEFEAKAPDRRVSPITNLTEPYMKFSRKFPFRFSASIASIFFMILLVMAAVMTV 471

Qy 519 ILYRAIMAIVVSRSNGTLLAAWASRIASLTGSVVNLVFILLSKIYVSLAHVLTWEMHR 578
      |:| | : : : : || | | | : | : | | : | : | | | |
Db 472 IVYRIVVKAIFAIDQEFISSYASIITSVTASMISLILIMILQILYERIAVWLTNLELHR 531

Qy 579 TQTKFEDAFTLVKFIFQVFNFYSSPVYIAFFKGRFVGYPGNYHTLFGV--RNEECAAGGCL 637
      |:|:| | | | | : | | | | | | | | | | | | | | | |
Db 532 TETEYEDSFTFKMYLFAFVNYYSTSFYIAFFKGRLPGTADYGRVFGIWRQECDPAGCM 591

Qy 638 IELAQELLVIMVGKQVINNMQEVLIPLKLGWQKFLRSKKRKAGASAGASQGWEDDYE 697
      || : : | || | | | : : | | : | : | | : | | | :
Db 592 QELFINIAITCMGKQFFNNFMELAMPVLMNFWRS--RTGRKEEKGSGK---GRYEQWEQDAD 647

Qy 698 LVPC--EGLFDEYLEMVLQFGFVTIFVAACPLAPLFA LLNNWVEIRLDARKFVCEYRRPV 755
      | || | ||| | : | | | | | | | | | | | | | | | |
Db 648 LADLGPRLGFLKEYLEMVQVQGFSTIFVAAPLAPLFA LLNNLVEVRLDAYKFISQLRRPV 707

Qy 756 AERAQDIGIWFHILAGLTHLAVISNAFLAFSSDFLPR---AYRWTRAHDLRGLNFTL 812
      |:| | | | | | : | | : : | : | | : | : | | | | | | : | : |
Db 708 AKRAQDIGAWYAILVTVGNLSVLTNALVIAFTSEFIPRQVFKYYYGGPEATLNGYTNWSL 767

Qy 813 A-----RAPSSFAAAHNRT-----CRYRAFRDDDGHSYQT--YWNL 846
      : || | | ||| | : | | | : | : | : |
Db 768 SYFNTVDMQNDKPTDPSYPRVGDEDTDPNYGLNVSVCRYRGNIDE--HYNVILDYWLW 825

Qy 847 LAIRLAFVIVFEHVVSFVGRLLDLLVPDIPESVEIKVKREYYLAKQAL 894
      :|:| | | : : | | : : | : | | : : | | | | | |
Db 826 IAIKLAFILLYEHFVLFTKFFVAYIIPDMPEFVNQIKRETYLGQQAL 873

```

RESULT 6

TM16D_HUMAN

ID TM16D_HUMAN

Reviewed;

955 AA.

AC Q32M45; Q8NAJ0; Q8NB39; Q8NB53;
 DT 29-MAY-2007, integrated into UniProtKB/Swiss-Prot.
 DT 06-DEC-2005, sequence version 1.
 DT 21-AUG-2007, entry version 17.
 DE Transmembrane protein 16D.
 GN Name=TMEM16D;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 OC Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORMS 2 AND 3).
 RC TISSUE=Brain, and Prostate;
 RX PubMed=14702039; DOI=10.1038/ngl285;
 RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
 RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
 RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
 RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahara K.,
 RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
 RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
 RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
 RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
 RA Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,
 RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
 RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O., Nomura Y.,
 RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
 RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
 RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
 RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
 RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
 RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
 RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
 RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
 RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
 RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
 RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
 RT "Complete sequencing and characterization of 21,243 full-length human
 RT cDNAs.";
 RL Nat. Genet. 36:40-45 (2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
 RX PubMed=15489334; DOI=10.1101/gr.2596504;
 RG The MGC Project Team;
 RT "The status, quality, and expansion of the NIH full-length cDNA
 RT project: the Mammalian Gene Collection (MGC).";
 RL Genome Res. 14:2121-2127 (2004).
 RN [3]
 RP IDENTIFICATION.
 RX PubMed=12739008;

RA Katoh M., Katoh M.;
 RT "FLJ10261 gene, located within the CCND1-EMS1 locus on human
 RT chromosome 11q13, encodes the eight-transmembrane protein homologous
 RT to C12orf3, C11orf25 and FLJ34272 gene products.";
 RL Int. J. Oncol. 22:1375-1381(2003).
 CC -!- SUBCELLULAR LOCATION: Membrane; Multi-pass membrane protein
 CC (Potential).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=1;
 CC IsoId=Q32M45-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q32M45-2; Sequence=VSP_025742;
 CC Name=3;
 CC IsoId=Q32M45-3; Sequence=VSP_025741, VSP_025743;
 CC Note=No experimental confirmation available;
 CC -!- SIMILARITY: Belongs to the TMEM16 family.

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 DR EMBL; AK091540; BAC03688.1; ALT_INIT; mRNA.
 DR EMBL; AK091591; BAC03704.1; -; mRNA.
 DR EMBL; AK092596; BAC03924.1; -; mRNA.
 DR EMBL; BC109308; AAI09309.1; -; mRNA.
 DR UniGene; Hs.58785; -.
 DR Ensembl; ENSG00000151572; Homo sapiens.
 DR HGNC; HGNC:23837; TMEM16D.
 DR MIM; 610111; gene.
 DR PharmGKB; PA134975112; -.
 DR ArrayExpress; Q32M45; -.
 DR InterPro; IPR007632; DUF590.
 DR PANTHER; PTHR12308; DUF590; 1.
 DR Pfam; PF04547; DUF590; 1.
 PE 2: Evidence at transcript level;
 KW Alternative splicing; Coiled coil; Glycoprotein; Membrane;
 KW Polymorphism; Transmembrane.
 FT CHAIN 1 955 Transmembrane protein 16D.
 FT /FTId=PRO_0000288650.
 FT TRANSMEM 353 373 Potential.
 FT TRANSMEM 425 445 Potential.
 FT TRANSMEM 506 526 Potential.
 FT TRANSMEM 548 568 Potential.
 FT TRANSMEM 596 616 Potential.
 FT TRANSMEM 716 736 Potential.
 FT TRANSMEM 769 789 Potential.
 FT TRANSMEM 886 906 Potential.
 FT COILED 918 953 Potential.
 FT CARBOHYD 824 824 N-linked (GlcNAc . .) (Potential).
 FT VAR_SEQ 1 433 Missing (in isoform 3).
 FT /FTId=VSP_025741.
 FT VAR_SEQ 19 54 EGGVDLQGYQLDMQILPDGPKSDVDFSEILNAIQEM -> V
 FT (in isoform 2).
 FT /FTId=VSP_025742.
 FT VAR_SEQ 466 512 Missing (in isoform 3).


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Db      685 GPERKISFPQWEKDYNLQPMNAYGLFDEYLEMILQFGFTTIFVAAPLAPLLALLNNIIE 744
Qy      740 IRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVISNAFLAFSSDFLPYRRYRW- 798
      ||||| ||| ::|||:| ||:|||||: || |: |:|:||||:| :|||:| | :
Db      745 IRLDAYKFVQTQWRRLPLASRAKDIGIWIYGILEGIGILSVITNAFVIAITSDFIPRLVYAYK 804
Qy      799 -----TRAHDLRGLFNFTLA-----RAPSSFAAAHNRTCRYAFRDD 835
      : |:| :|: | |: | |:| :||
Db      805 YGPCAGQGEAGQKCMVGYVNASLSVFRISDFENRSEPESDGSEFSGTPLKYCRYRDRDP 864
Qy      836 DGH-----YSQTYWNLLAIRLAFVIVFEHVVSFVGRLLDLLVPDIPESVEIKVKREYYLA 890
      |: :|:| | |||:| |||:| |: |: |:|:|: : :|:| ||
Db      865 PHSLVPGYTLQFVHVLAARLAFIIVFEHLVFCIKHLISYLIPDLPKDLDRMRREKYLI 924
Qy      891 KQALAENEVLFGTNGTKDEQPKGSELSSHW 920
      :: : | |: |: : | :|
Db      925 QEMMYEAELERLQKERKERKNGKAHHNEW 954

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RESULT 7

Q1AP35_STRPU

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ID      Q1AP35_STRPU              Unreviewed;          921 AA.
AC      Q1AP35;
DT      11-JUL-2006, integrated into UniProtKB/TrEMBL.
DT      11-JUL-2006, sequence version 1.
DT      24-JUL-2007, entry version 6.
DE      122 kDa protein TMEM16.
OS      Strongylocentrotus purpuratus (Purple sea urchin).
OC      Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC      Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
OC      Strongylocentrotus.
OX      NCBI_TaxID=7668;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RC      TISSUE=Testis;
RA      Galindo B.E., Vacquier V.D.;
RT      "Phylogeny of the TMEM16 Protein Family: Some Are Over Expressed in
RT      Cancer.";
RL      Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
CC      -----
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NoDerivs License
CC      -----
DR      EMBL; DQ020166; AAY82887.1; -, mRNA.
DR      UniGene; Spu.15325; -.
DR      InterPro; IPR007632; DUF590.
DR      PANTHER; PTHR12308; DUF590; 1.
DR      Pfam; PF04547; DUF590; 1.
PE      2: Evidence at transcript level;
SQ      SEQUENCE 921 AA; 106711 MW; C3F912A32528F059 CRC64;

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Query Match 30.8%; Score 1523; DB 2; Length 921;
 Best Local Similarity 37.8%; Pred. No. 1.5e-115;
 Matches 339; Conservative 159; Mismatches 305; Indels 94; Gaps 21;

Qy	61	QEEEDSTVLIDVSPPEAEKRGSYGSTAHASEPGGQAAACRAGSPAK-----	106
Db	26	QPDNAAV---ANPQEIEM-----AESHMGAPTDKEDQPLHEGSPAKKDDNKVNDLFFKDG	77
Qy	107	PRIADFLVWWEEDLKLDRQDQSDAARDTDMHRTWRETFLDNLRAAGLCV-----	155
Db	78	KRRIDFLVAY-----RKQSEEREKEKRVKK---RQNFEANLIDEGQLQLEYENSEGPEPK	128
Qy	156	-DQQDVQDGNITTVHYALLSASWAVLCYYAEDLRKLPLQELPNQASNWSAGLLAWLGIPN	214
Db	129	EDDPESHGDRGRT---FFVKVHAPWDLMTRYAEELKIKMPIEENNMEEPVNVFNCIDKLWTFP	186
Qy	215	VLLEVVPDVPPEYYSCRFVFNKLPRLFLGSDNQDITFTSTKRHQILFEILAKTPYGHEKKN	274
Db	187	ELSEEYVKPEPDVFTAPFIRDRASEFI-MESQDITFFPNNIRNRVVYEILERMYDANDPA	245
Qy	275	LLGIHQLLAEGVLSAAFPPLHDGPFKTP---PEGPQAPRLNQRQVLQFQHWARWGKWNKYQ	330
Db	246	KFGIDHLIANGSYFAAAYPLHEGDYKSKHSLTHGQP---NDRHLLYEWARPGRWYKKQ	301
Qy	331	PLDHVRRYFGEKVVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGSKDS	390
Db	302	PLDLIRRYFGEKIGIYFCWLGFYTEMLTWAGFVGLIVFLYGCISLSSVVVQIEICAGTDI	361
Qy	391	FEMCPLC-LDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLEYWKRSATLA	449
Db	362	I-MCPLCDKRCPYWTLSDSCFYSKLTYLFDNEATVFFACFMSLWATMFCFEWKRRQNTID	420
Qy	450	YRWDCSDYEDTEERPRPQFAASAPMTAPNPITGEDEPYFPERSARRMLAGSVVIVMVVA	509
Db	421	YDWDLFGFEEQEENIRPEFAKAPDRRVSPITNLTEPYMKFSRKFPFRFSASIASIFFMIL	480
Qy	510	VVVMCLVSIILYRAIMAVVSRSGNTLLAAWASRIASLTGSVVNLVFILILSKIYVSLAH	569
Db	481	LVMAAVMTVIVYRIVVKTAFIAIDQEFISSYASIIITSVTASMISLILIMILQILYERIAV	540
Qy	570	VLTRWEMHRTQTKFEDAFTLKVFIQFVNFIYSSPVYIAFFKGRFVGYPGNYHTLFGV-RN	628
Db	541	RLTNLELHRTETEYEDSFTFKMYLFAFVNYYSTSFYIAFFKGRGLPGTPADYGRVFGIWRQ	600
Qy	629	EECAAGGCLIELAQELLVIMVGKQVINNMQEVLIPLKLGWQKFLRLSKRRKAGASAGAS	688
Db	601	EECDPAGCMQELFINIAITMCGKQFFNNFMELAMPVLMNFWRS-RTGRKEEKSGK---GR	656
Qy	689	QGPWEDDYELVPC---EGLFDEYLEMLVQFGFVTIFVAACPLAPLALLNNWVEIRLDARK	746
Db	657	YEQWEQDADLADLGRGLFKEYLEMLVQFGFSTIFVAAFPLAPLALLNNLVEVRLDAYK	716
Qy	747	FVCEYRRPVAERAQDIGIWFHILAGLTHLAVISNAFLAFSSDFLPR---AAYRWTRAHD	803
Db	717	FISQLRRPVAKRAQDIGAWYAILVTGNNLSVLTNALVIAFTSEFIPRQVFKYYGGPEAT	776
Qy	804	LRGLFNFTLA-----RAPSSFAAAHNRT-----CRYAFRDDDGHY	839
Db	777	LNGYTNWLSLYFNTVDMQNSKPTDPSYPRVGEDTTDPNYGLNVSVCCIRYRGNYDE--HY	834

Qy 840 SQT--YWNLLAIRLAFVIVFEHVSVVGRLLDLLVPDIPESEIKVKREYYLAKQAL 894
 : | || :|||:|:|:| | : :||:| | : :||| || :|||
 Db 835 NVTLDYWLVIKLAFLILLYEHFVLFKFFVAYIIPDMPEFVKNQIKRETYLGQQAL 891

RESULT 8

A2AHE5_MOUSE

ID A2AHE5_MOUSE Unreviewed; 981 AA.
 AC A2AHE5;
 DT 20-FEB-2007, integrated into UniProtKB/TrEMBL.
 DT 20-FEB-2007, sequence version 1.
 DT 21-AUG-2007, entry version 6.
 DE Novel protein (B230324K02Rik).
 GN Name=RP23-300M9.6; ORFNames=RP23-300M9.6-002;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidea; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Smith M.;
 RL Submitted (JUL-2007) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Kay M.;
 RL Submitted (JUL-2007) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RA Phillimore B.;
 RL Submitted (JUL-2007) to the EMBL/GenBank/DDBJ databases.
 CC -----
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 CC -----
 DR EMBL; AL731700; CAM18325.1; -; Genomic_DNA.
 DR EMBL; AL731779; CAM18325.1; JOINED; Genomic_DNA.
 DR EMBL; BX005257; CAM18325.1; JOINED; Genomic_DNA.
 DR EMBL; AL731779; CAM25697.1; -; Genomic_DNA.
 DR EMBL; AL731700; CAM25697.1; JOINED; Genomic_DNA.
 DR EMBL; BX005257; CAM25697.1; JOINED; Genomic_DNA.
 DR EMBL; BX005257; CAM27817.1; -; Genomic_DNA.
 DR EMBL; AL731700; CAM27817.1; JOINED; Genomic_DNA.
 DR EMBL; AL731779; CAM27817.1; JOINED; Genomic_DNA.
 DR InterPro; IPR007632; DUF590.
 DR PANTHER; PTHR12308; DUF590; 1.
 DR Pfam; PF04547; DUF590; 1.
 PE 4: Predicted;
 SQ SEQUENCE 981 AA; 114568 MW; E851D80BC49F4977 CRC64;

Query Match 30.6%; Score 1512.5; DB 2; Length 981;
 Best Local Similarity 38.9%; Pred. No. 1.2e-114;
 Matches 333; Conservative 166; Mismatches 279; Indels 79; Gaps 25;

Qy 106 KPRIADFLVWEEDLKLRDQDQSAARDRTDMHRTWRETFDLNLRAGLCVDQDQVQDNGT 165

	: : : : : : : : : : : : : :	
Db	161 KKRI-DYILVYR-----KTNIQYDKRNTFEKNLRAEGLMLEKEPA-IANP	203
Qy	166 TVHYALLSASWAVLCYAEADRLRLKPLQ-----ELPNQASNWSAGLLAWLGIPNV	215
	: : : : : : : : : : : : : : :	
Db	204 DIMFIKIHIPWDTLCKYAEERLNIRVPRKKCCYYTDQKNKSKSRVQNYFKRIKKWMSQNP	263
Qy	216 LLE--VVPDV-PPEYSSCRFRVKNLPRFLGSDNQDTFFTSTKRHQILFEILAKTPY--GH	270
	: : : : : : : : : : : : : : : : : : : :	
Db	264 VLDKSAFPELEESDCYTGPFSSRARIHFI-INNKDTFFSNATRSRIVYHMLERTKYENGI	322
Qy	271 EKKNLGHIQLLAEGVLSAAFLHDGPFT----PPEGPQAPRLNQQRVLQHWARWGKW	326
	: : : : : : : : : :	
Db	323 SK---VGIRKLITNGSYIAAFPPEGAYKSSLPIKTHGPQ---NNRHLLYERWARWGMW	375
Qy	327 NKYQPLDHVRRYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCG	386
	: : : : : : : :	
Db	376 YKHQPLDLIRMYFGEKIGLYFAWLGWYTGMLIPAAVVGLCVFFYGLVTMNESQVSQEICK	435
Qy	387 SKDSFEMCPLC-LDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWKRKS	445
	: : : : : : : : : : : : : :	
Db	436 ATEVF-MCPLCDKNCSLQRLNDSCYAKVTYLFDNNGTVFFAIFMAIWAIVFLFVFWKRRR	494
Qy	446 ATLAYRWDCSDYEDTEERPRQFAAS-APMTAPNPITGEDEPYFPERSRARRMLAGSVVI	504
	: : : : : : :	
Db	495 SILTYTWDLIEWEEEEETLRQFEAKYYRMEVINPITGKPEHPQSSDKVTRLLVSVSGI	554
Qy	505 VVMVAVVVMCLVSIILYR-AIMAVVSRSGNTLLAAWASRIASLTGSV-VNLVFILILSK	562
	: : : : : : : : : : : : : : : : : : :	
Db	555 FFMISLVITAVFAVVVYRLVMEQFASFKNFVKQHW--QFATSGAAVCINFIIMLLNL	612
Qy	563 IYVSLAHVLRWEMHRTQTKFEDAFTLKVFIQFVNFIYSSPVYIAFFKGRFVGYPGNYHT	622
	: : : : : : : : : : :	
Db	613 AYEKIAYLLTNLEYPRTESEWENSFALKMFLFQFVNLSIFYIAFFLGRFVGHGPKYKN	672
Qy	623 LF-GVRNEECAAGGLIELAQELLVIMVGKQVINNMQEVLIPLKLGWVQKFLRLSKKRKA	681
	: : : : : : : : : :	
Db	673 LFERWRLEECHPSGCLIDLCLQMGVIMFLKQIWNNFMEGLGYPLQNWWSRHKI----KR	727
Qy	682 GASAGASQGPWEDDYELVP--CEGLFDEYLEMVLQFGVTFIVAAACPLAPLALLNNWVE	739
	: : : :	
Db	728 GIQ-DASIPQWENDWNLPNMNIHGLMDEYLEMVLQFGFTTIFVAAFLAPLALLLNNIIE	786
Qy	740 IRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVISNAFLAFSSDFLPRAYRW-	798
	: : : : : : : : :	
Db	787 IRLDAYKFVTQWRRRLPARATDIGIWLGLEGIGLAVITNAFVIAITSDYIPRFVYEEK	846
Qy	799 -----TRAHDLRGLNFTLARAP-SSFAAAHNRTCRYRAFR-----DDGHYSQTY	843
	: : : : : : : : : : : : :	
Db	847 YGPCANHVQKQENCLKGYVNNLSFFDLSELGMGKSGYCRYDRYRPPWSSKPYEFTLQY	906
Qy	844 WNLLAIRLAFVIVFEHVVSFVGRLLDLLVPDIPESVEIKVKREYLLAKQALAENEVLFGT	903
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Db	907 WHILARLAFIIVFEHLVFGIKSFIAYLIPDIPKGLRERIRREKYLQVQEMMYEAEEL---E	963
Qy	904 NGTKDEQPKGSELSSHW	920

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Db      964 HLQQRKSGQPIHHEW 980

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RESULT 9

TM16C_HUMAN

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ID      TM16C_HUMAN                      Reviewed;          981 AA.
AC      Q9BYT9;
DT      16-JAN-2004, integrated into UniProtKB/Swiss-Prot.
DT      01-JUN-2001, sequence version 1.
DT      24-JUL-2007, entry version 31.
DE      Transmembrane protein 16C.
GN      Name=TMEM16C; Synonyms=C11orf25; ORFNames=GENX-3947;
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC      Catarrhini; Homnidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      NUCLEOTIDE SEQUENCE [MRNA].
RA      Rosier M.F., Toselli E., Segurens-Soury B., Auffray C., Devignes M.D.;
RT      "Predominant brain expression and full-length characterization of a
RT      novel human 6.6-Kb transcript mapping at 11p14 in the telomeric part
RT      of WAGR locus.";
RL      Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
CC      -!- SUBCELLULAR LOCATION: Membrane; Multi-pass membrane protein
CC      (Probable).
CC      -!- SIMILARITY: Belongs to the TMEM16 family.
CC      -----
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NoDerivs License
CC      -----
DR      EMBL; AJ300461; CAC32454.1; -; mRNA.
DR      UniGene; Hs.91791; -.
DR      Ensembl; ENSG00000134343; Homo sapiens.
DR      KEGG; hsa:63982; -.
DR      HGNC; HGNC:14004; TMEM16C.
DR      MIM; 610110; gene.
DR      PharmGKB; PA25489; -.
DR      ArrayExpress; Q9BYT9; -.
DR      InterPro; IPR007632; DUF590.
DR      PANTHER; PTHR12308; DUF590; 1.
DR      Pfam; PF04547; DUF590; 1.
PE      2: Evidence at transcript level;
KW      Membrane; Transmembrane.
FT      CHAIN           1           981           Transmembrane protein 16C.
FT                                     /FTId=PRO_0000072565.
FT      TRANSMEM       398       420           Potential.
FT      TRANSMEM       471       490           Potential.
FT      TRANSMEM       553       575           Potential.
FT      TRANSMEM       590       612           Potential.
FT      TRANSMEM       642       664           Potential.
FT      TRANSMEM       759       781           Potential.
FT      TRANSMEM       809       831           Potential.
FT      TRANSMEM       904       926           Potential.

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A1A5Z4 DANRE

http://es.ScoreAccessWeb/GetItem.action?AppId=10552...4_083148_us-10-552-515-1.rup&ItemType=4&startByte=0 (25 of 41)10/10/2008 8:48:54 AM

Query Match 30.3%; Score 1500.5; DB 2; Length 900;
Best Local Similarity 38.0%; Pred. No. 1.1e-113;
Matches 323; Conservative 170; Mismatches 266; Indels 91; Gaps 20;

Qy 108 RIADFLVWVEEDLKLDRQQDSAARDRTDMHRTWRETFLDNLRAAGLCVDQDQVQDG-NTT 166
| ||| : : : : : | | || ||| : : : :
Db 49 RRIDFVLSYVDDEKGDKKAER-----RREFEANLEKAGLELETEDKSESDDRK 96

Qy 167 VHYALLSASAWLVCYYAEDLRCLKPL-----QELPNQASNWSAGLLAWLGIPNVLL 218
|| : || | || : ::| :| :| | |
Db 97 THYLKIHPWEVLATYADVLIKIKVPFKVSDIPKAREVP-----LEWLSHPFRLPE 146

219 VVPDVPEYYSCFRVKNLPRFLGSDNQDTFFTSTKRHQILFEILAKTPYGHE---KKNL 275
: |:: | :: || ::||| : :::: || : || | ::
147 NIMRPEPDYFTAPFDKSKVDFEL-IDDKDTFFPPSTRNRIVYYILTRCPYYKEDRKEKDK 205

Qy 276 LGIHQLLAEGVLSAAFLHDGPFKTPPEGPQAPRLNQRQVLFQHWARWGKWNKYQLPDHV 335
||::|| | ::||| : : | ::| |::||| : | ||: :
Db 206 TGINRLNNGTYTSAYPLHDCRYWKKAOODMOCE--SERYHLRYWARFLCFYKEOPLNLI 263

Qy 336 RRYFGKEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQLCGSK--DSFEM 393
:::|||: :||||||| | |||: | |: | :| ::| | |
Db 264 KKYYGEKIGIFYAFLGFTYTEMFYAAMGVICFVYGVLVSIEDNITSKEICDPKIGGMVM 323

Qy 394 CPLC-LDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWKRSATLAYRW 452
||| | :| :| | : ||| :|||:|:| :| | |:|:|:| | | |
Db 324 CPLCDKKCSYWKLNSTCLSSWOSHLEDNEGTVFFAFMFMGIWVTLEFFWKROARLEYEW 383

Qy 453 DCSDYEDTEE--RPRPQFAASAPMTAPNPITGEDEPYFPERSRARRMLAGSVVIVVMVAV 510
| |:|: :: :|:: | || | || | |: | :: :
Db 384 DLVDFEEEOOQLOIRPEYEOKCTGRRLNRITOEMEPYLPFPSKCARECLSGATVLEWTC 443

Qy 511 VVMCLVSIILYR----AIMAIVVSRSGNTLLAAWASRI-----ASLTGSVVNLVFILILS 561
:|:::| | | | | : : | | :| | :| | | | :
Db 444 IVACTMGVIAVRLAVYAAEASVMKDSSTSKIQLVGLITPOLATSVTASCNEVILILN 503

Qy 562 KIYVSLAHVLTRWEMHRTQTKEFDAFTLKVFIFQFVNFIYSSPVYIAFFKGRFVGYPGNYH 621
 :| :| :| |: :| ::| :|||:||||| :|:||||:|||||||
Db 504 ELYEHVAIWITDMEIPDKTHLEVENKLTMKMEMEFOFNYYSSCFYAFAFKKGFVGYPGNYS 563

Qy 622 TLFG----VRNEECAAGGCLIELAQELLVIMVGKQVINNMQEVLPKLGWQKFLRSK 677
:|| :||||| ||||| :||:| ||::| |:| |:| :: ||
Db 564 YMEGKWSLTNRNEECAPGGCLIELTTOILVIMAGKOMVGWVQFALPLVRNWW-----S 616

Qy 678 KRKAGASAGASQGPWEDDYELVPCE--GLFDEYLEMVLQFGFVTIFVAACPLAPLFPALLN 735
|| : :: || |:| |||||||:|:|:| | |
Db 617 SRKGSHPRESTYSRWODHDLDNESQEGLEYEYLEMVIOGFTILEVASDLPALIALEN 676

http://es.ScoreAccessWeb/GetItem.action?AppId=10552...4_083148_us-10-552-515-1.rup&ItemType=4&startByte=0 (27 of 41)10/10/2008 8:48:54 AM

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Qy      148 LRAAGLCV-----DQDDVQDGNNTTVHYALLSASWAVLCYYAEDLRKLPLQEL 375
      |  || :      :  || :      :  || :      |||::|::|::|
Db      110 LIDEGLQLLEYENSEGPEPKEDDPESHDRGT--FFVKVHAPWDLMTRYAELKIKMPIEN 167

Qy      196 PNQASNWSAGLLAWLGIPNVLLVVPDPPEYYSCFRFVNKLPRFLGSDNQDTFFTTSTKR 255
      :      :      :      :      :      :      :      :      :      :
Db      168 NMEEPVNWFNCIDKLWTFPELSEYVVKPEPDVFTAPFIRDRASEFI--MESQDTFFPNNIR 226

Qy      256 HQILFEILAKTPYCGHEKNLLGIHQLLAEGVLSAAFPPLHDGPFKTP----PEGPQAPRLN 311
      ::::|::| : |      || :| | |::|::| :|:      ||| |
Db      227 NRVVVEILERMRYDANDPTKFGIDHLIANGSYFAAYPLHEGDYKSKHSLTLHGPO----N 282

Qy      312 QRQVLFQHWARWGKWNKYQPLDHWRRYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVG 371
      | :::|::| || :| | |||| :| ||||| :|| ||||| | | || :||| |
Db      283 DRHLLYEWEARSGRWYKKQPLDLIRCYFGEKIGIFYCWLGFYTEMLTWAGFVGLVFLYLG 342

Qy      372 CFLVFSDIPTQELCGSKDSFEMCLPC--LDCPFWLLSSACALAQAGRLFDHGGTVFFSLFM 430
      | : : : ||:| | |||| |::| || :| : : ||| : |||: ||
Db      343 CISLPSSVVVQECICAGTDII--MCPLCDKRCPYWTLSDSCFCYSKLTYLFDNEATVFFACFM 401

Qy      431 ALWAVLLELYEYWKRSATLAYRWDCSDYEDTEERPRPQFAASAPMTAPNPITGEDEPYFPE 490
      :||| : :|||: |::| :| :| :| :| :| :| :| :| :| |
Db      402 SLWATMFCEFWKRRQNTIDYDWDLFGFEEQEENIRPEFEAKAPDRRVSPITNLPEQYMKF 461

Qy      491 RSRARRMLAGSVVIVVMVAVVMCLVSIILYRAIMAVVSRSGNTLLAAWASRIASLTGS 550
      | |      | : : :|::| : : :| : : :| : : :| : : :|
Db      462 SKRFRPFSTSVPTIAFMILLVMAAVMTVIVYRIVVKTAFIAIDQEFISSYASIITSVTAS 521

Qy      551 VVNLVFILILSKIYVSLAHVLTWRWEMHRTQTKFEDAFTLKVFIFQFVNFYSSPVYIAFFK 610
      ::::| :|| :| :| || :|||:|::|:| |::| |||:| | |||||
Db      522 MISLILIMILQILYERIAVWLTNLHLRHTETETEYEDSFTKMYLFAFVNYYSTSFYIAFFK 581

Qy      611 GRFVGYPGNYHTLFGV--RNEECAAGGCLIELAQELLVIMVGKQVINNMQEVLPKLGWGW 669
      || | : :| :|| : ||| || || : : ||| || | : :| | :|
Db      582 GRLPGTPADYGRVFGIWRQECDPAGCTQELFINIAITMCGKQFFNNFMELAMPVLMNFW 641

Qy      670 QKFRLSRKKRKAGASAGASQGPWEDDYELVPC--EGLFDEYLEMVLQFGFVTIFVAACPL 727
      : | : :|      || :| :| || |||||:|::| ||||| ||
Db      642 RS--RTGRKEEKGSGK---GRYEQWEQDADLADLGRGLFKEYLEMVVQFGFSTIFVAAPFL 697

Qy      728 APLFALLNNWVEIRLDARKFVCEYRRPAAERAQDIGIWFHILAGLTHLAVISNAFLLAFS 787
      ||||| |::|::| : : :|::|::| : : :|::|::| : : :|::|::| : : :|
Db      698 APLFALLNNLVEVRDAYKFISQLRRPVAKRAQDIGAWYAILVTVGNSVLTNALVIAFT 757

Qy      788 SDFLPR---AYYRWTRAHDLRGLFNFTLA-----RAPSSFAAHNRT----- 826
      |:|:| | | :| :| :|:| : | | |
Db      758 SEFIPRQVFKYKYGGPEATLNGYTNWLSYFNTVDMQNDSKPTDPSYPRVGDEDTTDPNY 817

Qy      827 -----CRYRAFRRDDGHYSQT--YWNLLAIRLAFVIVFEHVVSFVGRLLDLLVPDIPES 878
      |||| | : ||: | || :::|:|::|::| | : :||:|
Db      818 GLNVSVCRYRGNYDE--HYNVTLDYWLVIKLAFLILLYEHFVLFTKFFVAYIIPDMPEF 875

Qy      879 VEIKVKREYYLAKQAL 894
      | : :||| || :|||
Db      876 VKNOIKRETYLGOOAL 891

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RESULT 12

TM16A_MOUSE

ID TM16A_MOUSE Reviewed; 960 AA.
AC Q8BHY3; Q6P5C6; Q8BI26; Q99JK1;
DT 29-MAY-2007, integrated into UniProtKB/Swiss-Prot.
DT 29-MAY-2007, sequence version 2.
DT 24-JUL-2007, entry version 32.
DE Transmembrane protein 16A.
GN Name=Tmem16a;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RC STRAIN=C57BL/6J; TISSUE=Head, and Kidney;
RX PubMed=16141072; DOI=10.1126/science.1111204;
RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA Jakt M., Kanapin A., Katoh M., Kawasaki Y., Kelso J., Kitamura H.,
RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA Schoenbach C., Sekiguchi K., Sempere C.A., Seno S., Sessa L., Sheng Y.,
RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA Grimmer S.M., Teasdale R.D., Liu E.T., Brusica V., Quackenbush J.,
RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,

RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
 RA Hayashizaki Y.;
 RT "The transcriptional landscape of the mammalian genome.";
 RL Science 309:1559-1563(2005).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 2).
 RC STRAIN=C57BL/6, and Czech II; TISSUE=Eye, and Mammary tumor;
 RX PubMed=15489334; DOI=10.1101/gr.2596504;
 RG The MGC Project Team;
 RT "The status, quality, and expansion of the NIH full-length cDNA
 RT project: the Mammalian Gene Collection (MGC).";
 RL Genome Res. 14:2121-2127(2004).
 CC -!- SUBCELLULAR LOCATION: Cell membrane; Multi-pass membrane protein
 CC (By similarity). Cytoplasm (By similarity).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q8BHY3-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q8BHY3-2; Sequence=VSP_025672;
 CC -!- SIMILARITY: Belongs to the TMEM16 family.
 CC -!- SEQUENCE CAUTION:
 CC Sequence=BAC35051.1; Type=Miscellaneous discrepancy; Note=Wrong choice of frame;
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; AK028991; BAC26230.1; ALT_INIT; mRNA.
 DR EMBL; AK029329; BAC26398.1; ALT_INIT; mRNA.
 DR EMBL; AK052589; BAC35051.1; ALT_SEQ; mRNA.
 DR EMBL; BC006062; AAH06062.1; ALT_INIT; mRNA.
 DR EMBL; BC062959; AAH62959.1; -; mRNA.
 DR UniGene; Mm.26700; -.
 DR Ensembl; ENSMUSG00000031075; Mus musculus.
 DR MGI; MGI:2142149; Tmem16a.
 DR ArrayExpress; Q8BHY3; -.
 DR InterPro; IPR007632; DUF590.
 DR PANTHER; PTHR12308; DUF590; 1.
 DR Pfam; PF04547; DUF590; 1.
 PE 2: Evidence at transcript level;
 KW Alternative splicing; Cytoplasm; Glycoprotein; Membrane;
 KW Transmembrane.
 FT CHAIN 1 960 Transmembrane protein 16A.
 FT /FTId=PRO_0000288436.
 FT TOPO_DOM 1 333 Cytoplasmic (Potential).
 FT TRANSMEM 334 354 Potential.
 FT TOPO_DOM 355 402 Extracellular (Potential).
 FT TRANSMEM 403 423 Potential.
 FT TOPO_DOM 424 493 Cytoplasmic (Potential).
 FT TRANSMEM 494 514 Potential.
 FT TOPO_DOM 515 539 Extracellular (Potential).
 FT TRANSMEM 540 560 Potential.
 FT TOPO_DOM 561 581 Cytoplasmic (Potential).
 FT TRANSMEM 582 602 Potential.
 FT TOPO_DOM 603 705 Extracellular (Potential).
 FT TRANSMEM 706 726 Potential.

FT	TOPO_DOM	727	765	Cytoplasmic (Potential).
FT	TRANSMEM	766	786	Potential.
FT	TOPO_DOM	787	856	Extracellular (Potential).
FT	TRANSMEM	857	877	Potential.
FT	TOPO_DOM	878	960	Cytoplasmic (Potential).
FT	CARBOHYD	806	806	N-linked (GlcNAc. . .) (Potential).
FT	VAR_SEQ	448	451	Missing (in isoform 2).
FT				/FTId=VSP_025672.
SQ	SEQUENCE	960 AA;	110916 MW;	BFD0112FD310CE88 CRC64;

Query Match 30.1%; Score 1489; DB 1; Length 960;
 Best Local Similarity 37.5%; Pred. No. 1e-112;
 Matches 361; Conservative 170; Mismatches 303; Indels 128; Gaps 29;

Qy	26	GLYCRDQAAHAERWAMT--SETSSGSHCARSRLRRRAQEEDSTVLIDVSPPEAEKRGSYG	83
		: : : : : :	
Db	52	GLYFRDQKRVVDYILVYHHKRASG-----SRTLARRGLQNDMVL-----GTRS	94
Qy	84	STAHASEPGGQQAACRAGSPAKPRIADFLVWEEDLKLDRQQDQAARDRTDMHRTWRET	143
		: : : : : :	
Db	95	VRQDQPLPG--KGSVPVDAGSPEVP-----MDYHEDD-----KRFRREE	130
Qy	144	FLDNLRAAGLCVDQDQVQDGNNTTVH---YALLSASWAVLCYYAEDLRLKLPQLQELPNQAS	200
		: : : : : : : : : : :	
Db	131	YEGNLLAEAGLELE---NDEDTKIHGVGVKIHAPWHVLCREAEFLKLKMPKTKVYHISE	186
Qy	201	NWSAGLLAWLGIPNVLLLEVVPDVPPEYYSCFRVKNKLPFLGS-----DNQDTFFT	251
		: : : : : : : : : : :	
Db	187	--TRGLLK--TINSVLQKITDPIQPKVAEHRPQTKLRSYFFSREKQHLFDLTDSDRSDFFD	242
Qy	252	SKRKHQILFEILAKTPYHGEKKNLLGIHQLLAEGVLSAAFFLHDGPFKTPPEGPQAPRLN	311
		: : : : : : :	
Db	243	SKTRSTIVYEILKRTTCTKAKYS-MGITSLLANGVYSAAYPLHDGDY---EGDNV-EFN	296
Qy	312	QRQVLFQHWARWGKWKYQPLDHWRRYFGEKVALYFAWLGYFTGWLLPAAVVGTLVFLVG	371
		: : : : : : : : : : : :	
Db	297	DRKLLYEEWASYGVFYKQPIDLVRKYFGEKVGLYFAWLGAFTQMLIPASIVGVIVFLYG	356
Qy	372	CFLVFSDIPTQELCGSKDSFEMCPLC-LDCPFWLLSSACALAQAGRLFDHGGTVFFSLFM	430
		: : : : : : : : : :	
Db	357	CATVDENIPSMEMCDQRYNITMCPLCDKTCYWKMSACATARASHLFDNPATVFFSVFM	416
Qy	431	ALWAVLLLEYWKRKSATLAYRWDCSDYEDTEE----RPRPQFAA----SAPMTAPNPIT	481
		: : : : : : : :	
Db	417	ALWAATFMEHWKRMRLNRYWDLTGFEETEEAAVKDHPRAEYEAARVLEKSLRKESRNKET	476
Qy	482	GEDEPYFPERSRARMRLAGSVVIVVMVAVVVMCLVSIILYRAIMAIIVVSRSGNTLLAAWA	541
		: : : : : : : : : :	
Db	477	--DKVKLTWRDRFPAYFTNLVSIIFMIAVTFAIVLGVIIYRISTAAALAMNSSPSVRSNI	534
Qy	542	SRIASLTGSVVNLVFIILSKIYVSLAHVLTWRWEMHRTQTKFEDATLKVFIQFVNFYS	601
		: : : : : : : : : : : : : :	
Db	535	RVTVTATAVILNLVVIILLDEVYGCIARWLTAKIEVPKTEKSFEERLTFKAFLLKFVNSYT	594
Qy	602	SPVYIAFFKGRFVGYPGNYHTLF--GVRNEECAAGGCLIELAQELLVIMVGKQVI--NNMQE	659

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Db      595 PIFVYVAFPKGRFVGRPGDYVYIFRSFRMEECAPGGCLMELCIQLSIIMLGKQLIQNNLFE 654
Qy      660 VLIPKLGKWWQKFLRLSKRRKAGASAGASQGPWEDDYELVPCGLFDEYLEMVLQFGFVT 719
Db      655 IGIPKMKKFIRYLKLRQSPSDREEYVKKRQRYEVDFNLEPFFAGLTPEYMEMI IQFGFVT 714
Qy      720 IFVAACPLAPLALLNNWVEIRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVIS 779
Db      715 LFVASFPLAPLALLNNIIEIRLDAKFVTELRRPVAIRAKDIGIWNILRGVGLAVII 774
Qy      780 NAFLLAFSSDFLPRAYYRWTRAHD--LRGFLNFTLARAPSSF-----AAAHN----- 824
Db      775 NAFVISFTSDFIPRLVLYLMYSQNGTMHGFVNHTL---SSFNVSDFQNGTAPNDPLDLG 830
Qy      825 ---RTCRYRAFRD---DDGHY--SQTYWNLALAIRLAFVIVFEHVVSFVGRLLDLLVPDIP 876
Db      831 YEVQICRYKDYREPPWSEHKYDISKDFWAVLAARLAFVIVFQNLVFMFMSDFVDWVDPDIP 890
Qy      877 ESVEIKVKREYYL-----AKQALAENEVLFGTNGTKDEQPKGSELSSHWPFTVP 926
Db      891 KDISQIQIHKEKVLVLMVELFMREEQGKQLLDWTM-----EKEKPRDVPCNNH-SPTHP 942
Qy      927 KA 928
Db      943 EA 944

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RESULT 13

TM16A_HUMAN

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ID      TM16A_HUMAN                      Reviewed;          986 AA.
AC      Q5XXA6; Q8IYY8; Q8N7V3;
DT      29-MAY-2007, integrated into UniProtKB/Swiss-Prot.
DT      23-NOV-2004, sequence version 1.
DT      21-AUG-2007, entry version 18.
DE      Transmembrane protein 16A (Discovered on gastrointestinal stromal
DE      tumors protein 1) (Oral cancer overexpressed protein 2) (Tumor
DE      amplified and overexpressed sequence 2).
GN      Name=TMEM16A; Synonyms=DOG1, ORAOV2, TAOS2;
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC      Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), AND TISSUE SPECIFICITY.
RX      PubMed=16906560; DOI=10.1002/gcc.20371;
RA      Huang X., Godfrey T.E., Gooding W.E., McCarty K.S. Jr., Gollin S.M.;
RT      "Comprehensive genome and transcriptome analysis of the 11q13 amplicon
RT      in human oral cancer and syntenic to the 7F5 amplicon in murine oral
RT      carcinoma.";
RL      Genes Chromosomes Cancer 45:1058-1069 (2006).
RN      [2]
RP      NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 3).
RC      TISSUE=Testis;
RX      PubMed=14702039; DOI=10.1038/ng1285;

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RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,
RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O., Nomura Y.,
RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs.";
RL Nat. Genet. 36:40-45 (2004).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 2).
RC TISSUE=Testis;
RX PubMed=15489334; DOI=10.1101/gr.2596504;
RG The MGC Project Team;
RT "The status, quality, and expansion of the NIH full-length cDNA
RT project: the Mammalian Gene Collection (MGC).";
RL Genome Res. 14:2121-2127 (2004).
RN [4]
RP IDENTIFICATION, AND TOPOLOGY.
RX PubMed=12739008;
RA Katoh M., Katoh M.;
RT "FLJ10261 gene, located within the CCND1-EMS1 locus on human
RT chromosome 11q13, encodes the eight-transmembrane protein homologous
RT to C12orf3, C10orf25 and FLJ34272 gene products.";
RL Int. J. Oncol. 22:1375-1381 (2003).
RN [5]
RP SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RX PubMed=15215166;
RA West R.B., Corless C.L., Chen X., Rubin B.P., Subramanian S.,
RA Montgomery K., Zhu S., Ball C.A., Nielsen T.O., Patel R.,
RA Goldblum J.R., Brown P.O., Heinrich M.C., van de Rijn M.;
RT "The novel marker, DOG1, is expressed ubiquitously in gastrointestinal
RT stromal tumors irrespective of KIT or PDGFRA mutation status.";

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RL  Am. J. Pathol. 165:107-113(2004).
RN  [6]
RP  SUBCELLULAR LOCATION.
RX  PubMed=16261155; DOI=10.1038/sj.onc.1209203;
RA  Carles A., Millon R., Cromer A., Ganguli G., Lemaire F., Young J.,
RA  Wasylyk C., Muller D., Schultz I., Rabouel Y., Dembele D., Zhao C.,
RA  Marchal P., Ducray C., Bracco L., Abecassis J., Poch O., Wasylyk B.;
RT  "Head and neck squamous cell carcinoma transcriptome analysis by
RT  comprehensive validated differential display.";
RL  Oncogene 25:1821-1831(2006).
CC  -!- SUBCELLULAR LOCATION: Cell membrane; Multi-pass membrane protein.
CC      Cytoplasm.
CC  -!- ALTERNATIVE PRODUCTS:
CC      Event=Alternative splicing; Named isoforms=3;
CC      Name=1;
CC          IsoId=Q5XXA6-1; Sequence=Displayed;
CC      Name=2;
CC          IsoId=Q5XXA6-2; Sequence=VSP_025665, VSP_025668, VSP_025669;
CC          Note=No experimental confirmation available;
CC      Name=3;
CC          IsoId=Q5XXA6-3; Sequence=VSP_025666, VSP_025667, VSP_025668,
CC          VSP_025669, VSP_025670, VSP_025671;
CC          Note=No experimental confirmation available;
CC  -!- TISSUE SPECIFICITY: Broadly expressed with higher levels in liver
CC      and skeletal muscle.
CC  -!- SIMILARITY: Belongs to the TMEM16 family.
CC  -----
CC  Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC  Distributed under the Creative Commons Attribution-NoDerivs License
CC  -----
DR  EMBL; AY728143; AAU82085.1; -; mRNA.
DR  EMBL; AK097619; BAC05123.1; -; mRNA.
DR  EMBL; BC033036; AAH33036.2; -; mRNA.
DR  UniGene; Hs.503074; -.
DR  Ensembl; ENSG00000131620; Homo sapiens.
DR  HGNC; HGNC:21625; TMEM16A.
DR  MIM; 610108; gene.
DR  PharmGKB; PA128394678; -.
DR  ArrayExpress; Q5XXA6; -.
DR  InterPro; IPR007632; DUF590.
DR  PANTHER; PTHR12308; DUF590; 2.
DR  Pfam; PF04547; DUF590; 1.
PE  1: Evidence at protein level;
KW  Alternative splicing; Cytoplasm; Glycoprotein; Membrane; Polymorphism;
KW  Transmembrane.
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FT  TRANSMEM      334         354           Potential.
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FT  TRANSMEM      403         423           Potential.
FT  TOPO_DOM      424         519           Cytoplasmic (Potential).
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FT  TOPO_DOM      587         606           Cytoplasmic (Potential).

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FT	TRANSMEM	607	627	Potential.
FT	TOPO_DOM	628	731	Extracellular (Potential).
FT	TRANSMEM	732	752	Potential.
FT	TOPO_DOM	753	791	Cytoplasmic (Potential).
FT	TRANSMEM	792	812	Potential.
FT	TOPO_DOM	813	882	Extracellular (Potential).
FT	TRANSMEM	883	903	Potential.
FT	TOPO_DOM	904	986	Cytoplasmic (Potential).
FT	CARBOHYD	832	832	N-linked (GlcNAc. . .) (Potential).
FT	VAR_SEQ	1	116	Missing (in isoform 2). /FTId=VSP_025665.
FT	VAR_SEQ	1	28	Missing (in isoform 3). /FTId=VSP_025666.
FT	VAR_SEQ	29	36	GYLPSEGT -> MLTRPSQV (in isoform 3). /FTId=VSP_025667.
FT	VAR_SEQ	448	451	Missing (in isoform 2 and isoform 3). /FTId=VSP_025668.
FT	VAR_SEQ	476	501	Missing (in isoform 2 and isoform 3). /FTId=VSP_025669.
FT	VAR_SEQ	651	700	CAPGGCLMELCIQLSIIIMLGKQLIQNNLFEIGIPKMKKLIR YLKLLKQSQP -> VTEILFISGSPFCCLAYDLSTPCTWEKQL QHICSAKSSRFLSFLLETFLFP (in isoform 3). /FTId=VSP_025670.
FT	VAR_SEQ	701	986	Missing (in isoform 3). /FTId=VSP_025671.
FT	VARIANT	608	608	F -> S (in dbSNP:rs2186797). /FTId=VAR_032417.
FT	VARIANT	983	983	G -> R (in dbSNP:rs3740722). /FTId=VAR_032418.
FT	CONFLICT	801	801	N -> D (in Ref. 3; AAH33036).
FT	CONFLICT	948	948	W -> C (in Ref. 3; AAH33036).
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Query Match 29.9%; Score 1482; DB 1; Length 986;
 Best Local Similarity 36.8%; Pred. No. 4e-112;
 Matches 365; Conservative 162; Mismatches 302; Indels 164; Gaps 30;

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Db	52	GLYFRDGRKRVYDYLIVYHHKRPSTG-----NRTLVRVQHSSTP-----SGA 92
Qy	84	STAHASEPGGQQAACRAGSPAKPRIADFLVWEEDKLDRQQDQAARDRTDMHRTWRET 143
Db	93	RSVKQDHPPLPGKASLDAGSGEPP-----MDYHEDD-----KRFREE 130
Qy	144	FLDNLRAAGLCVDQDQVDGNTTVH---YALLSASWAVLCYYAEDRLRLKLPLQELPNQAS 200
Db	131	YEGNLEAGLELE---RDEDTKINGVGFVKIHAPWNLCREAEFLKLKMPKTKMYH--I 184
Qy	201	NWSAGLLAWLGIPIVNLLEVVPDPPEYYSR-----FRVNKLPRFLGSDNQDTFF 250
Db	185	NETRGLLK--KINSVLQKITDPIQPKVAEHRPQTMKRLSYFSPREKQHLFDLSD--KDSFF 241
Qy	251	TSTKRHQILFEILAKTPYGHEKKNLLGIHQLLAEGVLSAAFLHDGPFKTPPEGPQAPRL 310

Db 242 DSKTRSTIVYEILKRTTCTKAKYS-MGITSLLANGVYAAAYPLHGDGY-----NGENVEF 295

Qy 311 NQRQVLQFQHWARWGKWNKYQPLDHVRRYFGEKVYFAWLGFYTGWLLPAAVVGTLVFLV 370
| :|:|:|:| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

Db 296 NDRKLLYEEWARYGVFYKYQPIDLVRKYFGEKIGLYFAWLGVYQMLPIASIVGIIVFLY 355

Qy 371 GCFLVFSDIPTQELCGSKDSFEMCPLC-LDCPFWLLSSACALAQAGRLFDHGGTVFFSLF 429
| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

Db 356 GCATMDENIPMEMCDQRHNITMCPLCDKTCYSYWKMSACATARASHLFDNPATVFFSVF 415

Qy 430 MALWAVLLLEYWKRKSATLAYRWDSCDYEDTEE-----RPRPQFAA-----SAPMTAPNPI 480
| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

Db 416 MALWAATFMEHWKRQKRLNRYRDLTGFEETEEAVKDHPRAEYEARVLEKSLKKESSRNK- 474

Qy 481 TGEDEPYPPERS-----RARRMLAG-----SVVIVVMVAVVMV 513
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Db 475 --EKRRHIPEESTNKWKQRVKTAMAGVKLTDKVKLTWRDRFPAYLTNLVSIIFMIAVTFA 532

Qy 514 CLVSIILYRAIMAVVSRSGNTLLAAWASRIASLTGSSVNVLFILILSKIYVSLAHVLTR 573
:| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

Db 533 IVLGVIIYRISMAAALAMNSSPSVRSNIRVTVTATAVIINLVVILLDDEVYGCIARWLTK 592

Qy 574 WEMHRTQTKFEDAFTLKVFIFQFVNIFYSSPVYIAFFKGRFVGYPGNYHTLF-GVRNEECA 632
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Db 593 IEVPKTEKSFEERLIFKAPLLKFVNSYTPIFYVAFFKGRFVGPRGDIVYIFRSFRMEECA 652

Qy 633 AGGCLIELAQELLVIMVGKQVI--NNMQEVLIPKLGWQKFRRLRSKKRKAGASAGASQGP 691
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Qy 692 WEDDYELVPCEGLFDEYLEMVLQFGFVTIFVAACPLAPLFPALLNNWVEIRLDARKFVCEY 751
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Qy 752 RRPVAERAQDIGIWFHILAGLTHLAVISNAFLAFSSDFLPR--YYRWTRAHDLRGFLN 809
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| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

Db 889 ARLAFVIVFQNLVFMFMSDFVDWVIPDKDISQIHKVKLMVELFMREEQDKQQL--E 946

Qy 899 VLFNGTNGTKDEQP-----KGSELSSH 919
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Db 947 TWMEKERQKDEPPCNHNTKACPDLSLGPAPSH 979

RESULT 14

Q8CFW1_MOUSE

ID Q8CFW1_MOUSE

Unreviewed;

913 AA.

AC Q8CFW1;

DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.

DT 01-MAR-2003, sequence version 1.
 DT 24-JUL-2007, entry version 21.
 DE Transmembrane protein 16B.
 GN Name=Tmem16b;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidea; Muridae; Murinae; Mus.
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 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Eye;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ussdin T.B., Toshiyuki S., Carninci P., Prange C.,
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 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
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 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Eye;
 RG NIH MGC Project;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
 CC -----
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 DR EMBL; BC033409; AAH33409.1; -; mRNA.
 DR UniGene; Mm.333398; -.
 DR Ensembl; ENSMUSG00000038115; Mus musculus.
 DR MGI; MGI:2387214; Tmem16b.
 DR GO; GO:0016021; C:integral to membrane; IEA:UniProtKB-KW.
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 DR Pfam; PF04547; DUF590; 1.
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 KW Transmembrane.
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Qy     193  QEL-----PNQASNWSAGLLAWLGIPNVLLVVPDPPEYYSCRFVNKLP-----RF 240
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Qy     241  LGSDNQDTFFTTSTKRHQLFEILAKTPYGHEKKNLLGIHQLLAEGVLSAAPFLHDGPFKT 300
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Qy     301  PPEGPAQARLNQRQVLVQHWARWGKWKYQPLDHVRRYFGEKVALYFAWLGFYTGWLLPA 360
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Qy     361  AVVGLTVLVFGCFLVFSDIPTQELCGSKDSFEMCPLC-LDCPFWLLSSACALAQAGRLFD 419
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Db     288  SVIGVIVFLVGCATEIEDIPSKEMCDHQNAFTMCPLCDKSCDYNLSSACGTARASHLFD 347

Qy     420  HGGTVFFSLFMALWAVLLEIYWKRSATLAYRWDCSDYEDTEER---PRPQF----- 468
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Qy     469  -----AASAPMTAPNPITGE-DEPYFPERSRARRMLAGSVVIVVMVAVVVMCLVSIIL 520
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Qy     578  RTQTKFEDAFTLKVFIFQFVNFYSSPVYIAFFKGRFVGYPGNYHTLF-GVRNEECAAGGC 636
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Qy     696  YELVPCEGLFDEYLEMVLQFGFVTIFVAACPLAPLALLNNWVEIRLDARKFVCEYRRPV 755
      : | | | | | : | : | : | : | : | : | : | : | : |
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Db      763 FFNVSQQLKEGTQPENSQFDQEVQFCRFKDYREPPWAPNPYEFQYWSVLSARLAFVIIF 822

Qy      858 EHVVFVSVGRLLDLLVPDIPESVEIKVKRE 886
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RESULT 15

TM16B_HUMAN

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AC      Q9NQ90;
DT      16-JAN-2004, integrated into UniProtKB/Swiss-Prot.
DT      01-OCT-2000, sequence version 1.
DT      24-JUL-2007, entry version 35.
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GN      Name=TMEM16B; Synonyms=C12orf3;
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC      Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      NUCLEOTIDE SEQUENCE [MRNA].
RC      TISSUE=Retina;
RA      Lorenz B., White K.E., Econs M.J., Strom T.M.;
RT      "Transcripts in l2p13.3.";
RL      Submitted (FEB-2000) to the EMBL/GenBank/DBDJ databases.
CC      -!- SUBCELLULAR LOCATION: Membrane; Multi-pass membrane protein
CC      (Probable).
CC      -!- SIMILARITY: Belongs to the TMEM16 family.
CC      -----
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NoDerivs License
CC      -----
DR      EMBL; AJ272204; CAC01125.1; -; mRNA.
DR      UniGene; Hs.148970; -.
DR      Ensembl; ENSG00000047617; Homo sapiens.
DR      KEGG; hsa:57101; -.
DR      HGNC; HGNC:1183; TMEM16B.
DR      MIM; 610109; gene.
DR      PharmGKB; PA25504; -.
DR      LinkHub; Q9NQ90; -.
DR      ArrayExpress; Q9NQ90; -.
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DR      InterPro; IPR007632; DUF590.
DR      PANTHER; PTHR12308; DUF590; 1.
DR      Pfam; PF04547; DUF590; 1.
PE      2: Evidence at transcript level;
KW      Membrane; Polymorphism; Transmembrane.
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FT                                     /FTId=PRO_0000072564.
FT      TRANSMEM      360       382           Potential.
FT      TRANSMEM      535       557           Potential.
FT      TRANSMEM      577       599           Potential.

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Db      675  IQLSIIMLGKQLIQNNIFEIGVPKLK---KLFRKLKDETEAGETDSAHSKHPEQWDL DYS 731

Qy      698  LVPCEGLFDEYLEMVLQGFVTFVAAACPLAPL F ALLNNWEIRLDARKFVCEYRRPVAE 757
      | | || ||:|:|:| |||||:| | | | | | | | | | | | | | | | |
Db      732  LEPYTGLTPEYMEMIIQGFVTLFVASFPLAPV F ALLNNVIEVRLDAKKFVTELRRPDAV 791

Qy      758  RAQDIGIWFHILAGLTHLAVISNAFLLAFSSDF LPRAYYRWTRAHD--LRGFLNFTLA-- 813
      | :| | | | | | | | | : | : | | | | | | | | | | | | | | | |
Db      792  RTKDIGIWF DILSGIGKFSVISNAFVIAITSD FIPRLVYQYSYSHNGTLHG FVNHTLSFF 851

Qy      814  -----RAPSSF AAAHNRTCRYRAFRD----DDGHYSQTYWNLLAIRLAFVIVFEH 859
      : | : | | : : | : : | : | : | | | | | | | | | |
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Qy      860  VVFSVGRLLDLLVPDIPESVEIKVKRE-----YYLAKQALAENEVLFGTNGTKDEQPKG 913
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Db      912  LVMFLSVLVDWMIPDIPTDISDQIKKEKSL LVDFFLKE----EHEK LKLMDEPALRSPGG 967

Qy      914  SELSSHWTPTFTV PKA-SQL 931
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Db      968  GDRSRSR AASSAPSGSQL 986

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Search completed: June 24, 2008, 08:41:08

Job time : 524 secs

SCORE 3.0